

HUMAN xiap

```
1  gaaagggtggacaagtcctaatttcaagagaagatgacttttaacagttttgaaggatct 60
   M T F N S F E G S
61  aaaacttggtgtacctgcagacatcaataaggaagaattttagaagagtttaataga 120
   K T C V P A D I N K E E F V E E F N R
121 ttaaaaacttttgctaattttccaaagtggtagtcctgttttcagcatcaacactggcacga 180
   L K T F A N F P S G S P V S A S T L A R
181 gcagggtttctttatactggtgaaggagataccgtgcggtgcttttagttgtcatgcagct 240
   A G F L Y T G E G D T V R C F S C H A A
241 gtagatagatggcaatatggagactcagcagttggaagacacaggaagtatcccaaat 300
   V D R W Q Y G D S A V G R H R K V S P N
301 tgcagatttatcaacggcttttatcttgaaaatagtgccacgcagctctacaaattctggt 360
   C R F I N G F Y L E N S A T Q S T N S G
```

FIG. 1 (PAGE 1 OF 7)

HUMAN xiap

```

361  atccagaatggtcagtacaaagtgtgaaaactatctgggaagcagagatcattttgcctta
-----+-----+
a      I  Q  N  G  Q  Y  K  V  E  N  Y  L  G  S  R  D  H  F  A  L  -
421  gacaggccatctgagacacatgcagactatcttttgagaactgggcagggttagatatata
-----+-----+
a      D  R  P  S  E  T  H  A  D  Y  L  L  R  T  G  Q  V  D  I  -
481  tcagacaccatataccgagggaaccctgccatgtattgtgaagaagctagattaaagtcc
-----+-----+
a      S  D  T  I  Y  P  R  N  P  A  M  Y  C  E  E  A  R  L  K  S  -
541  tttcagaactggccagactatgctcacctaaccctaaagagagtagcaagtgtggactc
-----+-----+
a      F  Q  N  W  P  D  Y  A  H  L  T  P  R  E  L  A  S  A  G  L  -
601  tactacacagggtattggtgaccaagtgcagtgccttttgttgggtggaactgaaaaat
-----+-----+
a      Y  Y  T  G  I  G  D  Q  V  Q  C  F  C  C  G  G  K  L  K  N  -
661  tgggaacctgtgatcgctgctggtcagaacacacagcgacactttcctaattgcttcttc
-----+-----+
a      W  E  P  C  D  R  A  W  S  E  H  R  R  H  F  P  N  C  F  F  -
720

```

FIG. 1 (PAGE 2 OF 7)

HUMAN xiap

```
721  gtcttgccggaatcttaatatctcgaagtgaatctgatgctgtgagttctgataggaat 780
    +-----+-----+-----+-----+-----+-----+
a   V L G R N L N I R S E S D A V S S D R N -

781  ttcccaaatccaacaatcttccaagaataccatccatggcagattatgaagcacggatc 840
    +-----+-----+-----+-----+-----+-----+
a   F P N S T N L P R N P S M A D Y E A R I -

841  ttacttttgggacatggatatactcagttaacaaggagcagcttgcaagagctggattt 900
    +-----+-----+-----+-----+-----+-----+
a   F T F G T W I Y S V N K E Q L A R A G F -

901  tatgcttaggtgaagtgataaagtgaagtgctttcactgtggaggaggcctaactgat 960
    +-----+-----+-----+-----+-----+-----+
a   Y A L G E G D K V K C F H C G G G L T D -

961  tggaagcccagtgaaagacccttgggaaacaacatgctaaatgggtatccagggtgcaaatat 1020
    +-----+-----+-----+-----+-----+-----+
a   W K P S E D P W E Q H A K W Y P G C K Y -

1021 ctgttagaacagaagggacaagaatatataaacaatatcttaactcattcacttgag 1080
    +-----+-----+-----+-----+-----+-----+
a   L L E Q K G Q E Y I N N I H L T H S L E -
```

FIG. 1 (PAGE 3 OF 7)

HUMAN xiap

```
1081      gagtgtctgtaagaactactgagaaacaccatcactaactagaagaattgatgatacc 1140
      -----+-----+-----+-----+-----+
a      E C L V R T T E K T P S L T R R I D D T -
      atcttccaaaatcctatggtacaagaagctatactacgaatggggttcagtttcaaggacatt 1200
      -----+-----+-----+-----+-----+
a      I F Q N P M V Q E A I R M G F S F K D I -
      aagaaaaataatggaggaaaaaattcagatatctgggagcaactataaatacacttgaggtt 1260
      -----+-----+-----+-----+-----+
a      K K I M E E K I Q I S G S N Y K S L E V -
      ctggttgcagatctagtgaatgctcagaaagacagtatgcaagatgagtcgaagtcagact 1320
      -----+-----+-----+-----+-----+
a      L V A D L V N A Q K D S M Q D E S S Q T -
      tcattacagaaagagattagtagtgaagagcagctgaaggcgccctgcaaggaggagaagcttc 1380
      -----+-----+-----+-----+-----+
a      S L Q K E I S T E E Q L R R L Q E E K L -
      tgcaaaaatctgtatggatagaataatttgctatcgtttttgttccttgtggacatctagtc 1440
      -----+-----+-----+-----+-----+
```

FIG. 1 (PAGE 4 OF 7)

HUMAN xiap

```

a      C K I C M D R N I A I V F V P C G H L V      -
      acttgtaacaatgtgctgaagcagttgacaagtgccccatgtgctacacagtcattact      1500
1441 -----+-----+-----+-----+-----+-----+-----+-----+
a      T C K Q C A E A V D K C P M C Y T V I T      -
      ttcaagcaaaaaatttttatgtctttaactctaactctatagtaggcattgttattgttctt      1560
1501 -----+-----+-----+-----+-----+-----+-----+-----+
a      F K Q K I F M S *      -
      tattaccctgattgaatgtgtgatgtgaactgactttaagtaatcaggattgaattccat      1620
1561 -----+-----+-----+-----+-----+-----+-----+-----+
a      tagcatttgctaccaagtaggaaaaaaatgtacatggcagtggttttagttggcaatata      1680
1621 -----+-----+-----+-----+-----+-----+-----+-----+
a      atctttgaaatttcttgatttttcagggtatttagctgtattatccatttttttactgtta      1740
1681 -----+-----+-----+-----+-----+-----+-----+-----+
a      ttttaattgaaaccatagactaagaataagaagcatcatactataactgaacacaatgtgt      1800
1741 -----+-----+-----+-----+-----+-----+-----+-----+
a

```

FIG. 1 (PAGE 5 OF 7)

HUMAN xiap

1801 attcatagtatactgatttaatttcttaagtgtaagtgaattaatcatctggatttttat 1860
a -

1861 tcttttcagataggcttaacaaatggagcttctgtatatataaatgtggagattagagtta 1920
a -

1921 atctcccaatcacataaattgttttctgtgaaaaaggaaataaatgttccatgctggtg 1980
a -

1981 gaaagatagagattgttttagagggtgggtgtgtgttttaggattctgtccattttct 2040
a -

2041 tgtaaagnnataaacacgnacntgtgcgaaatatnttgtaaagtgatttgccattnttg 2100
a -

2101 aaagcgtaatttaatgataataactatcgcagcccaacatgtactgacatggaaagatgtca 2160
a -

FIG. 1 (PAGE 6 OF 7)

HUMAN xiap

2161 nagatatgttaagtgtataaatgcaagtggcnnnacactatgtatagtctgagccagatca 2220

a

2221 aagtatgtatgttnttaatatgcataagaacnanagatttgaaaagatatatacaccaaaactg 2280

a

2281 ttaaatgtggtttctcttcgggaggggggattgggggagggggcccgagagggtttta 2340

a

2341 naggggccttttcacttttcnacttttttcattttgttctgttcgnattttttataagtat 2400

a

2401 gtanaccccnnaagggttttatggnaactaacaatcagtaaacctaaccctcgactatcct 2460

a

2461 gtncctcttcctagggagctgtntgtttcccaaccaccaccttccctctgaacaaatgc 2520

a

2521 ctgagtgcctggggcacttttn 2540

a

FIG. 1 (PAGE 7 OF 7)

FIG. 2 (PAGE 1 OF 8)

HUMAN hiap-1

```
CTGGTGTGAATGACAAGGTCAAATGCTTCTGTGTGGCCTGATGCTGGATAACTGGAAAA 361
- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
C      G V N D K V K C C F C C G L M L D N W K R -

GAGGAGACAGTCCCTACTGAAAAGCATAAAAAGTTGTATCCTAGCTGCAGATTTCGTTTCAGA 421
- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
C      G D S P T E K K H K K L Y P S C R F V Q S -

GTCTAAATTCCCGTTAACAACTTGGAAGCTACCTCTCAGCCCTACTTTTCCTTCTTCAGTAA 481
- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
C      L N S V N N L E A T S Q P T F P S S V T -

CACATTCCACACACTCATTACTTCCGGGTACAGAAACAGTGATATTTCCGTGGCTCTT 541
- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
C      H S T H S L L P G T E N S G Y F R G S Y -

ATTCAAACCTCTCCATCAAATCCTGTAACTCCAGAGCAAATCAAGAAATTTCTGCCTTGA 601
- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
C      S N S P S N P V N S R A N Q E F S A L M -

TGAGAAGTTCCTACCCCTGTCCAATGAATAACGAAATGCCAGATTACTTTTCAGA 661
- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
C      R S S Y P C P M N N E N A R L L T F Q T -
```

FIG. 2 (PAGE 2 OF 8)

HUMAN hiap-1

```

721  CATGGCCATTGACTTTTCTGTCGCCAACAGATCTGCACGAGCAGGCTTTACTACATAG
      W P L T F L S P T D L A R A G F Y Y I G -
781  GACCTGGAGACAGAGTGGCTTGCTTTGCCCTGTGGTGGAAATTGAGCAATTGGGAACCGA
      P G D R V A C F A C G G K L S N W E P K -
841  AGGATAATGCTATGTCAGAACACCTGAGACATTTCCCAAATGCCCATTTATAGAAATC
      D N A M S E H L R H F P K C P F I E N Q -
901  AGCTTCAAGACACTTCAAGATACACAGTTTCTAATCTGAGCATGCAGACACATGCAGCCCC
      L Q D T S R Y T V S N L S M Q T H A A R -
961  GCTTTAAACATCTTTAACTGGCCCTCTAGTGTCTAGTTAATCCTGACGAGCTTGCAA
      F K T F F N W P S S V L V N P E Q L A S -
1021 GTCGGGGTTTTTATTATGTGGGTAACAGTATGATGTCAAAATGCTTTGCTGTGATGGTG
      A G F Y Y V G N S D D V K C F C C D G G -

```

FIG. 2 (PAGE 3 OF 8)

HUMAN hiap-1

```
1081 GACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGTTCAACATGCCAAGTGGTTTCCAA 1140
      L R C W E S G D D P W V Q H A K W F P R -
1141 GGTGTGAGTACTTGATAAGAATTAAAGGACAGGAGTTTCATCCGTCAGTTCAAGCCAGTT 1200
      C E Y L I R I K G Q E F I R Q V Q A S Y -
1201 ACCCTCATCTACTTGAACAGCTGCTATCCACATCAGACAGCCCAGGAGATGAAAAATGCAG 1260
      P H L L E Q L L S T S D S P G D E N A E -
1261 AGTCATCAATTATCCATTTGGAACTGGAGAAAGACCATTGAGAAGATGCCAATCATGATGA 1320
      S S I I H L E P G E D H S E D A I M M N -
1321 ATACTCCTGTGATTAAATGCTGCCGTGGAATGGGCTTTAGTAGAAGCCTGGTAAACAGA 1380
      T P V I N A A V E M G F S R S L V K Q T -
1381 CAGTTCAGAGAAAAATCCTAGCAACTGGAGAGAATTATAGACTAGTCAATGATCTTGTGT 1440
      V Q R K I L A T G E N Y R L V N D L V L -
```

FIG. 2 (PAGE 4 OF 8)

HUMAN hiap-1

1441	TAGACTTACTCAATGCAGAAGATGAATAAGGGAAGAGAGAGAGAAAGCAACTGAGG	1500
C	D L L N A E D E I R E E R A T E E -	
1501	AAAAAGAATCAAAATGATTATTATTAAATCCGGAAGAAATAGAAATGGCACTTTTTCACACATT	1560
C	K E S N D L L L I R K N R M A L F Q H L -	
1561	TGACTTGTGTAATCCCAATCCTGGATAGTCTACTACTGCCGGAATTATTAAATGAACAAG	1620
C	T C V I P I L D S L L T A G I I N E Q E -	
1621	AACATGATGTTATTAACAGAAGACACAGACGCTTTACAAGCAAGAGAACTGATTGATA	1680
C	H D V I K Q K T Q T S L Q A R E L I D T -	
1681	CGATTTTAGTAAAGGAAATATTGCAGCCCACTGTATTCAGAAACTCTCTGCAAGAAGCTG	1740
C	I L V K G N I A A T V F R N S L Q E A E -	
1741	AAGCTGTGTTATATGAGCATTTATTGTGCAACAGGACATAAAATATATTTCCACAGAAG	1800
C	A V L Y E H L F V Q Q D I K Y I P T E D -	

FIG. 2 (PAGE 5 OF 8)

HUMAN hiap-1

```
1801 ATGTTTCAGATCTACCAAGTGAAGAACAAATTGCGGAGACTACCAGAAGAAAGAACATGTA 1860
-----+-----+-----+-----+-----+-----+-----+-----+
C V S D L P V E E Q L R R L P E E R T C K -
1861 AAGTGTGTATGGACAAAGAGTGTCACATAGTGTTTATTCCTTGTGGTCATCTAGTAGTAT 1920
-----+-----+-----+-----+-----+-----+-----+-----+
C V C M D K E V S I V F I P C G H L V V C -
1921 GCAAAGATTGTGCTCCTTCTTAAGAAAGTGTCCTATTGTAGGAGTACAATCAAGGGTA 1980
-----+-----+-----+-----+-----+-----+-----+-----+
C K D C A P S L R K C P I C R S T I K G T -
1981 CAGTTCGTACATTTCTTTCATGAAGAAGAACCAACCATCGTCTAAACTTTAGAAATTAAT 2040
-----+-----+-----+-----+-----+-----+-----+-----+
C V R T F L S *
2041 TTATTAAATGTATTATAACTTTAACTTTTATCCTAATTGGTTTCCTTAAATTTTATT 2100
-----+-----+-----+-----+-----+-----+-----+-----+
C TATTCAACTCAAAAACATTTGTTTGTGTAACATATTATATATGTATCTAAACCATA 2160
-----+-----+-----+-----+-----+-----+-----+-----+
C
```

FIG. 2 (PAGE 6 OF 8)

HUMAN hiap-1

```

2161 TGAACATATATTTTAGAAACTAAGAGAAATGATAGGCTTTTGTCTTATGAACGAAAAA 2220
-----+-----+-----+-----+-----+-----+-----+
-
2221 GAGGTAGCCACTACAAACACAAATATTCAATCCAAATTCAGCATTATTGAAATTGTAAAGTG 2280
-----+-----+-----+-----+-----+-----+-----+
-
2281 AAGTAAACTTAAGATATTTGAGTTAACCTTTAAGAAATTTTAAATATTTTGGCATTGTAC 2340
-----+-----+-----+-----+-----+-----+-----+
-
2341 TAATACCGGGAACATGAAGCCAGGTGTGGTGTATGTACCTGTAGTCCCAGGCTGAGGCA 2400
-----+-----+-----+-----+-----+-----+-----+
-
2401 AGAGAAATTACTTGAGCCCAGGAGTTTGAATCCATCCTGGGCAGCATACTGAGACCCCTGCC 2460
-----+-----+-----+-----+-----+-----+-----+
-
2461 TTTAAACXACAGXACCXAAACCAACACCAGGACACATTTCTCTGTCTTTTGTGAT 2520
-----+-----+-----+-----+-----+-----+-----+
-

```

FIG. 2 (PAGE 7 OF 8)

HUMAN hiap-1

```
2521 CAGTGTCCATACATCGAAGGTGTCATATATGTTGAATCACATTTTAGGGACATGGTGT 2580
-----+-----+-----+-----+-----+-----+-----+-----+
2581 TTTTATAAAGAAATTCTGTGAGXAAAAATTTAATAAAGCAACCXAAATTACTCTTAAAAAA 2640
-----+-----+-----+-----+-----+-----+-----+-----+
2641 AAAAAAAAAAAAACTCGAGGGGCCCGTACCAAT 2676
-----+-----+-----+-----+-----+-----+-----+-----+
```

FIG. 2 (PAGE 8 OF 8)

HUMAN hiap-2

```
a      1  TTAGGTTACCTGAAGAGTTACTACAACCCCAAGAGTGTGTTCTAGTAGTATCTTGG
      1  -----+-----+-----+-----+-----+-----+-----+-----+
a      61  TAAATTCAGAGAGATACTCATCCTACCTGAATATAAACTGAGATAAATCCAGTAAGAAG
      61  -----+-----+-----+-----+-----+-----+-----+-----+
a     121  TGTAGTAAATCTACATAAGAGTCTATCATGATTTCTTTTGTGGTGAATCTTAGTT
     121  -----+-----+-----+-----+-----+-----+-----+-----+
a     181  CATGTGAAGAAATTTCATGTGAATGTTTGTAGCTATCAAAACAGTACTGTCACTACTCATG
     181  -----+-----+-----+-----+-----+-----+-----+-----+
a     241  CACAAACTGCCCTCCCAAGACTTTTCCCAAGGTCCCTCGTATCAAAACATTAAGAGTATA
     241  -----+-----+-----+-----+-----+-----+-----+-----+
a     301  H K T A S Q R L F P G P S Y Q N I K S I
          ATGGAAGATAGCAGCATCTTGTGAGATTGACAAACAGCAACAACAATAATGAAGTAT
          -----+-----+-----+-----+-----+-----+-----+-----+
a     360  M E D S T I L S D W T N S N K Q K M K Y
          -----+-----+-----+-----+-----+-----+-----+-----+
```

FIG. 3 (PAGE 1 OF 7)

HUMAN hiap-2

```

361      GACTTTTCCTGTGAACTCTACAGAAATGTCTACATATTCAACTTCCCCCGGGGTGCCT
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      D F S C E L Y R M S T Y S T F P A G V P -
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
421      GTCTCAGAAAGGAGTCTTGCTCGTCTGGTGTGTTTATTATACTGGTGTGAATGACAAGGTC
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      V S E R S L A R A G F Y Y T G V N D K V -
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
481      AAATGCTTCTGTGTGGCCTGATGCTGGATAACTGGAACTAGGAGACAGTCCTATTCAA
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      K C F C C G L M L D N W K L G D S P I Q -
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
541      AAGCATAAACAGCTATATCCTAGCTGTAGCTTTATTCAGAAATCTGGTTTCAGCTAGTCTG
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      K H K Q L Y P S C S F I Q N L V S A S L -
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
601      GGATCCACCTCTAAGAATACGTCTCCAATGAGAAACAGTTTTCACATTATCTCTCCC
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      G S T S K N T S P M R N S F A H S L S P -
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
661      ACCTTGGAACATAGTAGCTTGTTTCAGTGGTCTTACTCCAGCCTTCCCAAACCCCTCTT
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      T L E H S S L F S G S Y S S L P P N P L -
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
720

```

FIG. 3 (PAGE 2 OF 7)

HUMAN hiap-2

```

721  AATTCTAGAGCAGTTGAAGACATCTCTTCATCGAGGACTAACCCCTACAGTTATGCAATG 780
      N S R A V E D I S S S R T N P Y S Y A M -
841  AGTACTGAAGAAGCCAGATTCTTACCTACCATATGTGGCCATTAACTTTTGTGCACCA 840
      S T E E A R F L T Y H M W P L T F L S P -
      TCAGAAATTGGCAAGAGCTGGTTTTTATTATATAGGACCCTGGAGATAGGGTAGCCCTGCTTT 900
      S E L A R A G F Y Y I G P G D R V A C F -
961  GCCTGTGGTGGGAAGCTCAGTAACTGGGAACCAAGGATGATGCTATGTCAAGAACCCGG 960
      A C G G K L S N W E P K D D A M S E H R -
1021 AGGCATTTCCCAACTGTCCATTTTGGAAAATCTCTAGAAACTCTGAGGTTAGCATT 1020
      R H F P N C P F L E N S L E T L R F S I -
      TCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACAATTATGTACTGGCCATCT 1080
      S N L S M Q T H A A R M R T F M Y W P S -

```

FIG. 3 (PAGE 3 OF 7)

HUMAN hiap-2

```
1081 AGTGTTCCAGTTCAGCCTGAGCAGCTTGCAAGTGCTGGTTTTATTATGTGGTGC GAAT 1140
      S V P V Q P E Q L A S A G F Y Y V G R N -
1141 GATGATGTC AAATGCTTTGGTTGTGATGGTGGCTTGAGGTGTGGGAATCTGGAGATGAT 1200
      D D V K C F G C D G G L R C W E S G D D -
1201 CCATGGGTAGAAACATGCCCAAGTGGTTTCCAAGGTGTGAGTCTTGTGATACGAATGAAAGGC 1260
      P W V E H A K W F P R C E F L I R M K G -
1261 CAAGAGTTTGTGATGAGATTCAAGGTAGATATCCTCATCTTCTTGAACAGCTGTTGTCA 1320
      Q E F V D E I Q G R Y P H L L E Q L L S -
1321 ACTTCAGATACCACTGGAGAGAAAATGCTGACCCACCAATTATTCATTTTGACCTGGA 1380
      T S D T T G E E N A D P P I I H F G P G -
1381 GAAAGTTCTTCAGAAAGATGCTGTGTCATGATGAATACACCTGTGGTTAAATCTGCCTTGGA 1440
      E S S S E D A V M M N T P V V K S A L E -
```

FIG. 3 (PAGE 4 OF 7)

Title: ANTISENSE IAP OLIGONUCLEOTIDES AND USES THEREOF
Applicant(s): Robert G. Korneluk et al.
Filing Date: August 7, 2003 Serial No.:
Page 20 of 67 Customer No.: 21559

FIG. 3 (PAGE 5 OF 7)

HUMAN hiap-2

```
1801 AACATCTTCAAAACTGTCTAAAGAAATTGACTCTACATTGTATAAGAACTTATTTGTG 1860
      N I F K N C L K E I D S T L Y K N L F V -
1861 GATAAGAATATGAAGTATATTCCAACAGAAAGATGTTTCAGGTCTGTCACTGGAAGAACAA 1920
      D K N M K Y I P T E D V S G L S L E E Q -
1921 TTGAGGAGGTTGCAAGAAGAACGAACTTGTAAGTGTTGATGGACAAAGAGTTTCTGTGT 1980
      L R R L Q E E R T C K V C M D K E V S V -
1981 GTATTATTCCTTGTCATCTGGTAGTATGCCAGGAATGTGCCCTTCTCTAAGAAAA 2040
      V F I P C G H L V V C Q E C A P S L R K -
2041 TGCCCTATTTCAGGGGTATAATCAAGGGTACTGTTTCGTACATTTCTCTTAAAGAAA 2100
      C P I C R G I I K G T V R T F L S *
2101 ATAGTCTATATTTAACCTGCATAAAAAGGTCTTTAAAAATATGTTGAACACTTGAAGCC 2160
      a
```

FIG. 3 (PAGE 6 OF 7)

HUMAN hiap-2

2161 ATCTAAAGTAAAAAGGGAATTATGAGTTTTC AATTAGTAACATTCATGTTCTAGTCTGC 2220
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
a -

2221 TTTGGTACTAATAATCTTGTTTCTGAAAAGATGGTATCATATATTTAATCTTAATCTGTT 2280
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
a -

2281 TATTTACAAGGGAAGATTTATGTTTGGTGAAC TATATTAGTATGTATGTGTACCTAAGGG 2340
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
a -

2341 AGTAGCGTCXCTGCTTGTTATGCATCATTTTCAGGAGTTACTGGATTTGTTGTTCTTTCAG 2400
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
a -

2401 AAAGCTTTGAAXACTAAATTATAGTGTAGAAAAGAACTGGAACCAGGAACCTCTGGAGTT 2460
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
a -

2461 CATCAGAGTTATGGTGCCGAAATTGTCCTTTGGTGCTTTTCACTTGTTGTTTAAATAAGGA 2520
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
a -

2521 TTTTCTCTTATTTCTCCCCCTAGTTTGTGAGAAACATCTCAATAAAGTGCTTTAAAG 2580
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
a -

FIG. 3 (PAGE 7 OF 7)

GACACTCTGCGGGCGGGCCCTCCTCCGGGACCTCCCCCTCGGGAACCGTCGCC

1 -----+-----+-----+-----+-----+-----+ 60

[illegible]

GAGAAAGATGACTTTTAAACAGTTTGAAGGAAGTACTAGAACTTTTGTACTTGCAGACACCAAT
121 -----+-----+-----+-----+-----+-----+-----+ 180

M T F N S F E G T R T F V L A D T N

181-----+-----+-----+-----+ 240

K K D E E F F V E E F F N R L K T F A N F P S

AGTAGTCCTGTTTCAGCATCAACATTGGCCGAGCTGGGTTCTTTATACCGTGAAGGA
241 -----+-----+-----+-----+-----+-----+-----+ 300

S S P V S A S T L A R A G F L Y T C E G

GACACCGTGC AATGTTTCAGTTGTCTCATGCCGCAATAGATAGATGGCAGTATGGAGACTCA
-----+-----+-----+-----+-----+-----+-----+ 360

D T V Q C F S C H A A I D R W Q Y G D S

FIG. 4 (PAGE 1 OF 6)

MOUSE xiap

```

361      GCTGTTGGAAGACACAGGAGAAATATCCCCCAAATGCGAGATTATCAATGGTTTATTTT      420
      A V G R H R R I S P N C R F I N G F Y F -
421      GAAAATGGTGCTGCACAGTCTACAAATCCTGGTATCCAAATGCCAGTACAAATCTGAA      480
      E N G A A Q S T N P G I Q N G Q Y K S E -
481      AACTGTGTGGGAAATAGAAATCCTTTTGCCCCCTGACAGGCCACCTGAGACTCATGCTGAT      540
      N C V G N R N P F A P D R P P E T H A D -
541      TATCTCTTGAGAACTGGACAGGTTGTAGATATTTTCAGACACCATATACCCGAGGAACCT      600
      Y L L R T G Q V V D I S D T I Y P R N P -
601      GCCATGTGTAGTGAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCCGACTATGCTCAT      660
      A M C S E E A R L K S F Q N W P D Y A H -
661      TTAACCCAGAGAGTTAGCTAGTGTGCTGGCCCTCTACTACACAGGGGCTGATCAAGTG      720
      L T P R E L A S A G L Y Y T G A D D Q V -

```

FIG. 4 (PAGE 2 OF 6)

MOUSE xiap

```

721  CAATGCTTTGTGGGAAACTGAAAAATTGGGAACCCCTGTGATCGTGCCTGGTCA 780
      Q C C C G G K L K N W E P C D R A W S -
841  GAACACAGGAGACACTTTCCCAATTGCTTTTGTGTTTGGGCCGGAACGTTAATGTTCGA 840
      E H R R H F P N C F F V L G R N V N V R -
      AGTGAATCTGGTGTGAGTCTGATAGGAATTCCCAAAATTCACAACTCTCCAAGAAAT 900
      S E S G V S S D R N F P N S T N S P R N -
901  CCAGCCATGGCAGAAATATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACTCAGTT 960
      P A M A E Y E A R I V T F G T W I Y S V -
      AACAGGAGCAGCTTGCAAGAGCTGGATTATGCTTTAGGTGAAGCGGATAAAGTGAAG 1020
      N K E Q L A R A G F Y A L G E G D K V K -
1021 TGCTTCCACTGTGGAGGGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGGACCAG 1080
      C F H C G G G L T D W K P S E D P W D Q -

```

FIG. 4 (PAGE 3 OF 6)

MOUSE xiap

```
1081 CATGCTAAGTGCTACCCAGGTGCAAAATACCTATTGGATGAGAAGGGCAAGAAATATATA 1140
      H A K C Y P G C K Y L L D E K G Q E Y I -
1141 AATAATATTCATTAAACCCATCCACTTGAGGAATCTTTGGGAAGAACTGCTGAAAAACA 1200
      N N I H L T H P L E E S L G R T A E K T -
1201 CCACCGCTAACTAAAAATCGATGATACCATCTTCCAGAATCCTATGGTGCAAGAAGCT 1260
      P P L T K K I D D T I F Q N P M V Q E A -
1261 ATACGAATGGGATTTAGCTTCAAGGACCTTAAGAAAAACAATGGAAGAAAAATCCAAACA 1320
      I R M G F S F K D L K K T M E E K I Q T -
1321 TCCGGAGCAGCTATCTATCACTTGAGGTCCTGATTGCAGATCTTGTGAGTGCTCAGAAA 1380
      S G S S Y L S L E V L I A D L V S A Q K -
1381 GATAATACGAGGATGAGTCAAGTCAAACTTCATTGCAGAAAGACATTAGTACTGAAGAG 1440
      D N T E D E S S Q T S L Q K D I S T E E -
```

FIG. 4 (PAGE 4 OF 6)

MOUSE xiap

```
1441 CAGCTAAGGCGCCTACAAGAGGAGAAAGCTTTCCTCCAAAATCTGTATGGATAGAAATATTGCT 1500
a Q L R R L Q E E K L S K I C M D R N I A -
1501 ATCGTTTTTTTCCCTTGTTGGACATCTGGCCACTTGTAAACAGTGTGCAGAACGAGTTGAC 1560
a I V F F P C G H L A T C K Q C A E A V D -
1561 AAATGTCCCATGTGCTACACCGTCATTACGTTCAACCAAAAATTTTATGTCCTTAGTGG 1620
a K C P M C Y T V I T F N Q K I F M S * -
1621 GGCACCATGTATGTTCTTCTTCTCTAATTGAATGTGTAATGGGAGCGAACTTTAAG 1680
a TAATCCCTGCATTTCATTCATTCATCCCTGCTGTTTCCAAATGGAGACCAATGCTAAC 1740
a AGCACTGTTTCCGCTCTAAACATTCAATTTCTGGATCTTTCGAGTTATCAGCTGTATCATTT 1800
a
```

FIG. 4 (PAGE 5 OF 6)

MOUSE xiap

1801	TAGCCAGTGTTT	ACTCGATTGAAACCTTAGACAGAGAGCATT	TTTATAGC	TTTTCACAT	1860
	-----+	-----+	-----+	-----+	
					-
1861	GTATATTGGTAGTACACTGACTTGATTCTATATGTAAAGTGAATTCATCACCTGCATGTT	1920			
	-----+	-----+	-----+	-----+	
					-
1921	TCATGCCCTTTTGCCATAAGCTTAACAAATGGAGTGTTCTGTATAAGCATGGAGATGTGATG	1980			
	-----+	-----+	-----+	-----+	
					-
1981	GAATCTGCCCCAATGACTTTAATTGGCTTATTGTAAACACGGAAGAACTGCCCCACGCTG	2040			
	-----+	-----+	-----+	-----+	
					-
2041	CTGGGAGGATAAAGATTGTTTATAGATGCTCAGTCTCTGTGTTTAGGATTCTGCCCATTTA	2100			
	-----+	-----+	-----+	-----+	
					-

a

a

a

a

FIG. 4 (PAGE 6 OF 6)

M-hiap-1

```

1  GAATTCGGGAGACCTACACCCCGAGATCAGAGGTGCTGCGGTCAGAGCCTAG 60
   +-----+-----+-----+-----+-----+-----+
61  GAAGTGGGCTGCGGTATCAGCCTAGCAGTAAACCGACCAGAAGCCATGCACAAACTAC 120
   +-----+-----+-----+-----+-----+-----+
121 ATCCCCAGAGAAAGACTTGTCCTTCCCTCCCTGTCATCTCACCATGAACATGGTTCAA 180
   +-----+-----+-----+-----+-----+-----+
                                   M N M V Q
181 GACAGCGCCTTTCTAGCCAAGCTGATGAAGAGTGCTGACACCTTTGAGTTGAAGTATGAC 240
   +-----+-----+-----+-----+-----+-----+
   D S A F L A K L M K S A D T F E L K Y D
241 TTTTCCTGTAGCTGTACCGATTGTCCACGTATTCAGCTTTTCCCGGGAGTTCCTGTG 300
   +-----+-----+-----+-----+-----+-----+
   F S C E L Y R L S T Y S A F P R G V P V
301 TCAGAAAGGAGTCTGGCTCGTGGCTTTTACTACACTGGTGCCCAATGACAAGGTCAAG 360
   +-----+-----+-----+-----+-----+-----+
   S E R S L A R A G F Y Y T G A N D K V K
361 TGCTTCTGTGGCCTGATGTAGACAACTGGAACAAGGGACAGTCCCATGGAGAAG 420
   +-----+-----+-----+-----+-----+-----+
   C F C C G L M L D N W K Q G D S P M E K

```

FIG. 5 (PAGE 1 OF 6)

M-hiap-1

```
421 CACAGAAAGTTGTACCCAGCTGCAACTTTGTACAGACTTTGAATCCAGCCAACAGCTG
    H R K L Y P S C N F V Q T L N P A N S L - 480
481 GAAGCTAGTCCTCGGCCTTCTCTTCCCTTCCACGGCGATGAGCACCATGCCCTTTGAGCTTT
    E A S P R P S L P S T A M S T M P L S F - 540
541 GCAAGTTCTGAGAATACTGGCTATTTCAGTGGCTTACTCGAGCTTCCCTCAGACCCT
    A S S E N T G Y F S G S Y S S F P S D P - 600
601 GTGAACTTCCGAGCAATCAAGATTGTCCTGCTTTGAGCACAAAGTCCCTACCACCTTGCA
    V N F R A N Q D C P A L S T S P Y H F A - 660
661 ATGAACACAGAGAGCCAGATTACTCACCTATGAAACATGGCCATTGCTTTCTGTCA
    M N T E K A R L L T Y E T W P L S F L S - 720
721 CCAGCAAAGCTGGCCAAAGCAGGCTTCTACTACATAGGACCTGGAGATAGAGTGGCCTGC
    P A K L A K A G F Y Y I G P G D R V A C - 780
```

FIG. 5 (PAGE 2 OF 6)

M-hiap-1

```

781 TTTGCGTGGGAACTGAGCAACTGGGAACGTAAGGATGATGCTATGTCAGAGCAC
    F A C D G K L S N W E R K D D A M S E H
840
841 CAGAGGCATTTCCCGAGCTGTCGGTTCTTAAAGACTTGGGTCAGTCTGCTTCGAGATAC
    Q R H F P S C P F L K D L G Q S A S R Y
900
901 ACTGTCTTAACCTGAGCATGCAGACACACGAGCCCGTATTAGAACATTCTCTAACTGG
    T V S N L S M Q T H A A R I R T F S N W
960
961 CCTTCTAGTGCACTAGTTCAATCCAGGAACTTGCAAGTGGGGCTTTATTATACAGGA
    P S S A L V H S Q E L A S A G F Y Y T G
1020
1021 CACAGTGATGATCAAGTGTTTATGCTGTGATGGTGGGCTGAGGTGCTGGGAATCTGGA
    H S D D V K C L C C D G G L R C W E S G
1080
1081 GATGACCCCTGGGTGGAACATGCCAAGTGGTTTCCAAGGTGTGAGTACTTGCTCAGAATC
    D D P W V E H A K W F P R C E Y L L R I
1140
1141 AAAGGCCAAGAATTGTGAGCCCAAGTTCAAGCTGGCTATCCTCATCTACTTGAGCAGCTA
    K G Q E F V S Q V Q A G Y P H L L E Q L
1200

```

FIG. 5 (PAGE 3 OF 6)

M-hiap-1

1201	TTATCTACGTCACTCCCAGAAGATGAGATGCAGACGCAATCGTGCAATTTGGC	1260
	L S T S D S P E D E N A D A A I V H F G	-
	CCTGGAGAAAAGTTCGGAAGATGTCGTCAATGATGAGCACGCCCTGTGGTTAAAGCAGCCTTG	1320
1261	P G E S S E D V V M M S T P V V K A A L	-
	GAAATGGGCTTCAGTAGGAGCCTGGTGAGACAGACGGTTCAGTGGCAGATCCTGGCCACT	1380
1321	E M G F S R S L V R Q T V Q W Q I L A T	-
	GGTGAGAACTACAGGACCGTCAGTGACCTCGTTATAGGCTTACTCGATGCAGAAGACGAG	1440
1381	G E N Y R T V S D L V I G L L D A E D E	-
	ATGAGAGAGGAGCAGATGGAGCAGGCGCGGAGGAGGAGTCAGATGATCTAGCACTA	1500
1441	M R E E Q M E Q A A E E E S D D L A L	-
	ATCCGGAAGAACAAAATGGTGCTTTTCCAAACATTTGACGTGTGTGACACCAATGCTGTAT	1560
1501	I R K N K M V L F Q H L T C V T P M L Y	-

FIG. 5 (PAGE 4 OF 6)

M-hiap-1

```
1561 TGCCTCCTAAGTGCAAGGCCATCACTGAACAGGAGTGCAATGCTGTGAAACAGAAACCA + 1620
      C L L S A R A I T E Q E C N A V K Q K P -
1621 CACACCTTACAAGCAAGCACACTGATTGATACTGTGTAGCAAAGAAACACTGCAGCA + 1680
      H T L Q A S T L I D T V L A K G N T A A -
1681 ACCTCATTCAAGAACTCCCTTCGGGAAATTGACCCCTGCGTTATACAGATATATTGTG + 1740
      T S F R N S L R E I D P A L Y R D I F V -
1741 CAACAGGACATTAGGAGTCTTCCACAGATGACATTGCAGCTCTACCAATGGAAGAACAG + 1800
      Q Q D I R S L P T D D I A A L P M E E Q -
1801 TTGCGGCCCTCCCGAGGACAGAAATGTGTAAGTGTGTATGGACCGAGAGGTATCCATC + 1860
      L R P L P E D R M C K V C M D R E V S I -
1861 GTGTTCAATCCCTGTGGCCATCTGGTCGTGCAAGAACTGCGCTCCCTCTCTGAGGAAG + 1920
      V F I P C G H L V V C K D C A P S L R K -
```

FIG. 5 (PAGE 5 OF 6)

M-hiap-1

1921	TGTCCCATCTGTAGAGGACCATCAAGGCACAGTGGCACATTTCTCTCTGAACAAGA	1980
	C P I C R G T I K G T V R T F L S *	
1981	CTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCACGTGTCACTCCCAGTTCCAT	2040
2041	TCGGAACTTGAGGCCAGCCTGGATAGCACGAGACACCGCCAAACACACAATATAAACAT	2100
2101	GAAAACTTTTGTCTGAAGTCAAGAAATGAATGAATTACTTATATAATAATTTTAATTGGT	2160
2161	TTCCTTAAAGTGCTATTGTGTTCCCAACTCAGAAAATTGTTTCTGTAAACATATTTACA	2220
2221	TACTACCTGCATCTAAAGTATTTCATATATTTCATATATTCAGATGTCATGAGAGGGTTT	2280
2281	TGTTCTTGTTCCTGAAAAGCTGGTTTATCATCTGATCAGCATATATACTGCCAACGGGCAG	2340
2341	GGCTAGAATCCATGAACCAAGCTGCAAGATCTCAGCGCTAAATAAGGCGGAAAGATTGG	2400
2401	AGAAACGAAAGGAAATTCTTTCCTGTCCCAATGTATACTCTTCAGACTAATGACCTCTTCC	2460
2461	TATCAAGCCCTTCTA	

FIG. 5 (PAGE 6 OF 6)

M-hiap-2

```

CTGTGGTGAGATCTATTGTCCAAGTGGTGAGAACTTCATCTGGAAGTTTAAGCGGTCA
1  -----+-----+-----+-----+-----+-----+ 60
GAAATACTATTACTACTGACAAAAGTGTCTCCAGAGACTCGCCCAAGGTACCTTA
61  -----+-----+-----+-----+-----+-----+ 120
CACCCAAAAGTAAACGTATAATGGAGAAAGACACAATCTTGTCAAATTGGACAAAGGA
121 -----+-----+-----+-----+-----+-----+ 180
      M E K S T I L S N W T K E
GAGCGAAGAAAAATGAAGTTTGACTTTTCGTGTGAACCTCTACCGAATGTCTACATATTC
181 -----+-----+-----+-----+-----+-----+ 240
      S E E K M K F D F S C E L Y R M S T Y S
AGCTTTTCCAGGGAGTTCCTGTCTCAGAGAGGAGTCTGGCTCGTGGCTTTTATTA
241 -----+-----+-----+-----+-----+-----+ 300
      A F P R G V P V S E R S L A R A G F Y Y
TACAGGTGTGAATGACAAAGTCAAGTGCTTCTGTGGCCTGATGTTGGATAACTGGAA
301 -----+-----+-----+-----+-----+-----+ 360
      T G V N D K K V K C F C C G L M L D N W K
ACAAGGGACAGTCTCTGTTGAAAAGCACAGACAGTTCTATCCAGCTGCAGCTTTGTACA
361 -----+-----+-----+-----+-----+-----+ 420
      Q G D S P V E K H R Q F Y P S C S F V Q

```

Title: ANTISENSE IAP OLIGONUCLEOTIDES AND USES THEREOF

Applicant(s): Robert G. Korneluk et al.

Filing Date: August 7, 2003

Serial No.:

Page 35 of 67 Customer No.: 21559

FIG. 6 (PAGE 1 OF 6)

M-hiap-2

```
421  GACTCTGCTTTCAGCCAGTCTGCAGTCTCCATCTAAGAAATATGTCTCTGTGAAAAGTAG
      T L L S A S L Q S P S K N M S P V K S R
480  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      A T T T G C A C A T T C G T C A C C T C T G G A A C G A G T G C A T T C A C T C C A A C C T G T G C T C T A G C C C
481  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      F A H S S P L E R G G I H S N L C S S P
540  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      T C T T A A T T C T A G A G C A G T G G A A G A C T T C T C A T C A A G G A T G G A T C C C T G C A G C T A T G C C A T
541  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      L N S R A V E D F S S R M D P C S Y A M
600  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      G A G T A C A G A A G A G C C A G A T T T C T T A C T A C A G T A T G T G C C T T T A A G T T T T C T G T C A C C
601  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      S T E E A R F L T Y S M W P L S F L S P
660  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      A G C A G A G C T G C C A G A G C T G G C T T C T A T T A C A T A G G C C T G G A C A G A G G T G C C T G T T T
661  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      A E L A R A G F Y Y I G P G D R V A C F
720  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      T G C C T G T G T G G A A A C T G A G C A A C T G G A A C C A A G G A T T A T G C T A T G T C A G A G C A C C G
721  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      A C G G K L S N W E P K D Y A M S E H R
780  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
```

FIG. 6 (PAGE 2 OF 6)

M-hiap-2

```
781 CAGACATTTCCCCACTGTCCTCAATTTCTGGAATACTTCAGAAACACAGAGTTTAGTAT
-----+-----+-----+-----+-----+-----+-----+
R H F P H C P F L E N T S E T Q R F S I - 840

841 ATCAAATCTAAGTATGCAGACACACTCTGCTCGATTGAGGACATTTCTGTAAGCCACC
-----+-----+-----+-----+-----+-----+-----+
S N L S M Q T H S A R L R T F L Y W P P - 900

901 TAGTGTTCCCTGTTCAAGCCGAGCAGCTTGCAAGTCTGCTGATTCTATTACGTGGATCGCAA
-----+-----+-----+-----+-----+-----+-----+
S V P V Q P E Q L A S A G F Y Y V D R N - 960

961 TGATGATGTCAGTGCCCTTTGTTGTGATGGTGGCTTGAGATGTTGGGAACCTGGAGATGA
-----+-----+-----+-----+-----+-----+-----+
D D V K C L C C D G G L R C W E P G D D - 1020

1021 CCCCTGGATAGAACGCCAAATGGTTTCCAAGGTGTGAGTTCTTGATACGGATGAAGGG
-----+-----+-----+-----+-----+-----+-----+
P W I E H A K W F P R C E F L I R M K G - 1080

1081 TCAGGAGTTTGTGATGAGATTCAAGCTAGATATCCTCACTTCTTGAGCAGCTGTTGTC
-----+-----+-----+-----+-----+-----+-----+
Q E F V D E I Q A R Y P H L L E Q L L S - 1140
```

FIG. 6 (PAGE 3 OF 6)

M-hiap-2

```

1141  CACTTCAGACACCCAGAGAGAAAATGCTGACCCCTACAGAGACAGTGGTGCATTTTGG
      T S D T P G E E N A D P T E T V V H F G - 1200
1201  CCCTGGAGAAAGTTCGAAAGATGTCGTCAATGATGAGCACGCCCTGTGGTTAAAGCAGCCTT
      P G E S S K D V V M M S T P V V K A A L - 1260
1261  GGAAATGGGCTTCAGTAGGAGCCCTGGTGAGACAGACGCTTCAGCGCAGATCCTGGCCAC
      E M G F S R S L V R Q T V Q R Q I L A T - 1320
1321  TGGTGAGAACTACAGGACCGTCAATGATATTGTCTCAGTACTTTTGAATGCTGAAGATGA
      G E N Y R T V N D I V S V L L N A E D E - 1380
1381  GAGAAGAGAAGAGAGAGAAAGACAGACTGAAGAGATGGCATCAGGTGACTTATCACT
      R R E E E K E R Q T E E M A S G D L S L - 1440
1441  GATTCGGAAGAAATAGAACCCCTCTTTCAACAGTTGACACATGTCTTCCTATCCTCGGA
      I R K N R M A L F Q Q L T H V L P I L D - 1500

```

FIG. 6 (PAGE 4 OF 6)

M-hiap-2

```

1501 TAATCTTTCTTGAGGCCAGTGTAATTACAAAACAGGAACATGATATTATTAGACAGAAAAC
      N L L E A S V I T K Q E H D I I R Q K T
1560
1561 ACAGATACCCCTTACAAGCAAGAGAGCTTATTGACACCCGTTTGTAGTCAAGGGAATGCTGC
      Q I P L Q A R E L I D T V L V K G N A A
1620
1621 AGCCAACATCTTCAAAAACCTCTCTGAAGGGAATTGACTCCACGTTATATGAAAACCTTATT
      A N I F K N S L K G I D S T L Y E N L F
1680
1681 TGTGGAAGAAATATGAAGTATATCCAAACAGACGTTTCAGGCTTGTCATTGGAAGA
      V E K N M K Y I P T E D V S G L S L E E
1740
1741 GCAGTTGCGGAGATTACAAGAAGAACGAACTTGCAAGTGATGGACAGAGAGGTTTC
      Q L R R L Q E E R T C K V C M D R E V S
1800
1801 TATTGTGTTCAATCCGTGTGTCATCTAGTAGTCTGCCAGGAATGTCCCCCTTCTCTAAG
      I V F I P C G H L V V C Q E C A P S L R
1860

```

FIG. 6 (PAGE 5 OF 6)

M-hiap-2

```
1861  GAAGTCCCCATCTGCAGGGGACAATCAAGGGACTGTGCGCACATTTCTCTCATGAGT 1920
      K C P I C R G T I K G T V R T F L S *
1921  GAAGAAATGGTCTGAAAGTATTGTTGGACATCAGAAGCTGTCAGAACAAAGAAATGAACTAC 1980
      TGATTTTCAGCTCTTCAGCAGGACATTTCTACTCTCTTCAAGATTAGTAATCTTGCTTTAT 2040
1981  GAAGGGTAGCATTGTATATTTAAGCTTAGTCTGTTGCAAGGGAAGGCTCTATGCTGTTGAG 2100
2041  CTACAGGACTGTGTCGTCTCCAGAGCAGGAGTTGGGATGCTTGGTGTATGTCCTTCAGGA 2160
2101  CTTCTTGGGATTGGGAATTGGGGAAAGCTTTGGAATCCAGTGATGTGGAGCTCAGAAA 2220
2161  TCCTGGAACCACTGACTCTGCTACTCAGTAGATAGGGTACCCCTGTACTTCTTGGTGCTTT 2280
2221  TCCAGTCTGGGAAATAAGGAGGAATCTGCTGCTGGTAAATAATTGCTGGATGTGAGAAAT 2340
2281  AGATGAAAGTGTTTCGGGTGGGGCGGTGCATCAGTGTAGTGTGTCAGGATGTATGCAG 2400
2341  GCCAAACACTGTGTAG
2401  ----- 2416
```

FIG. 6 (PAGE 6 OF 6)

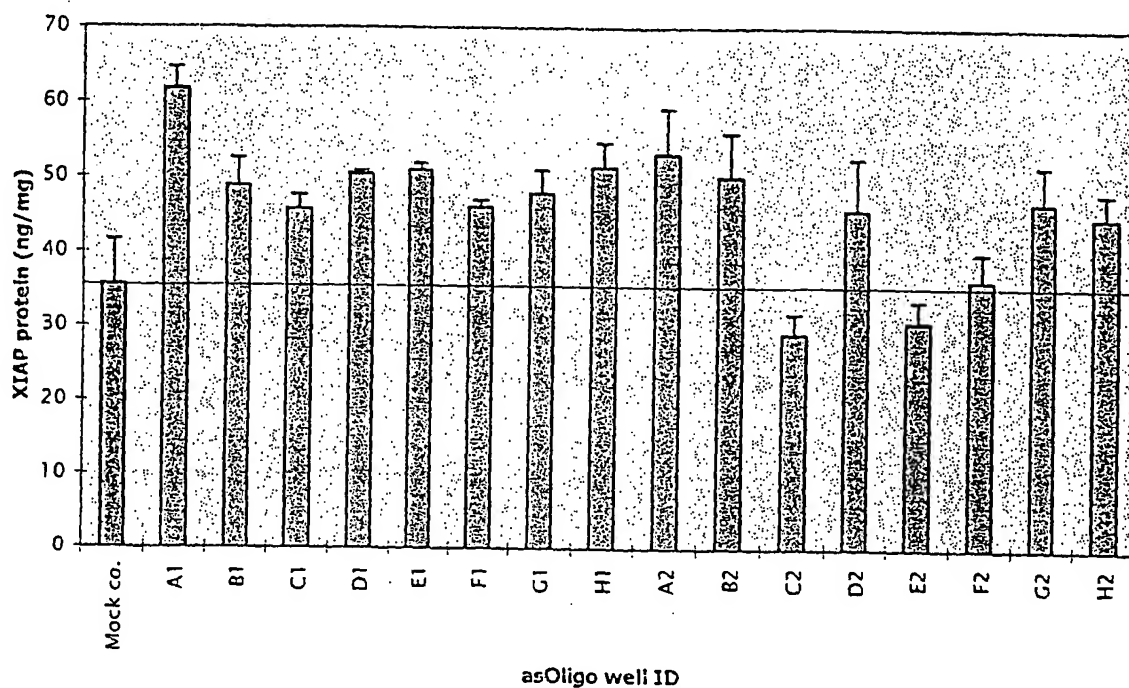


Fig. 7A

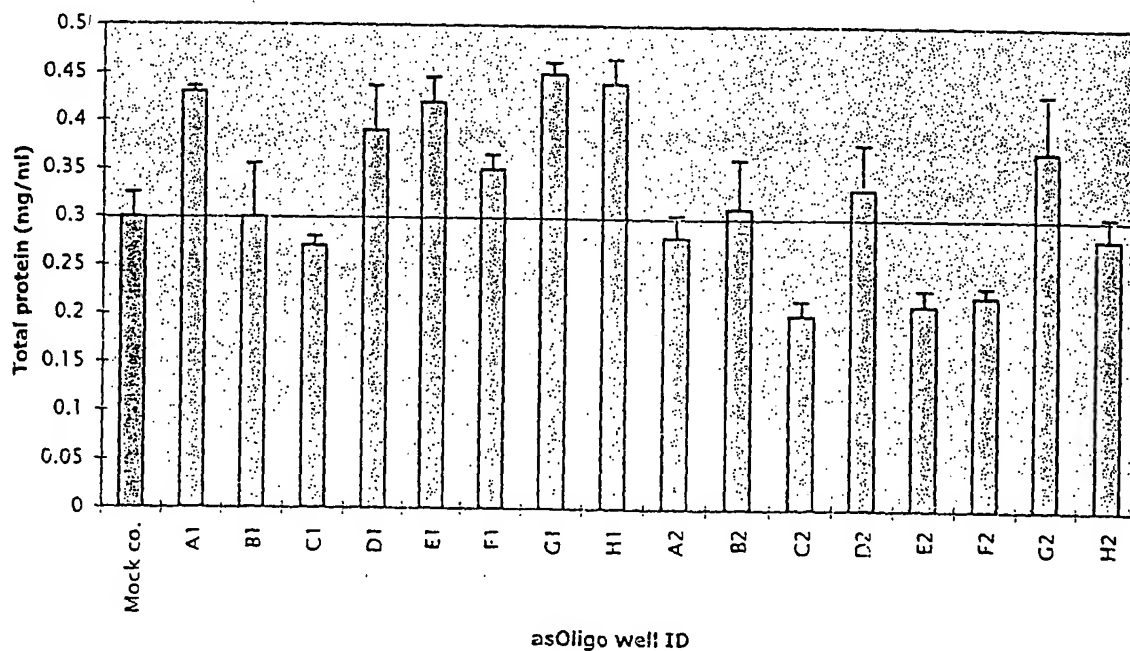


Fig. 7B

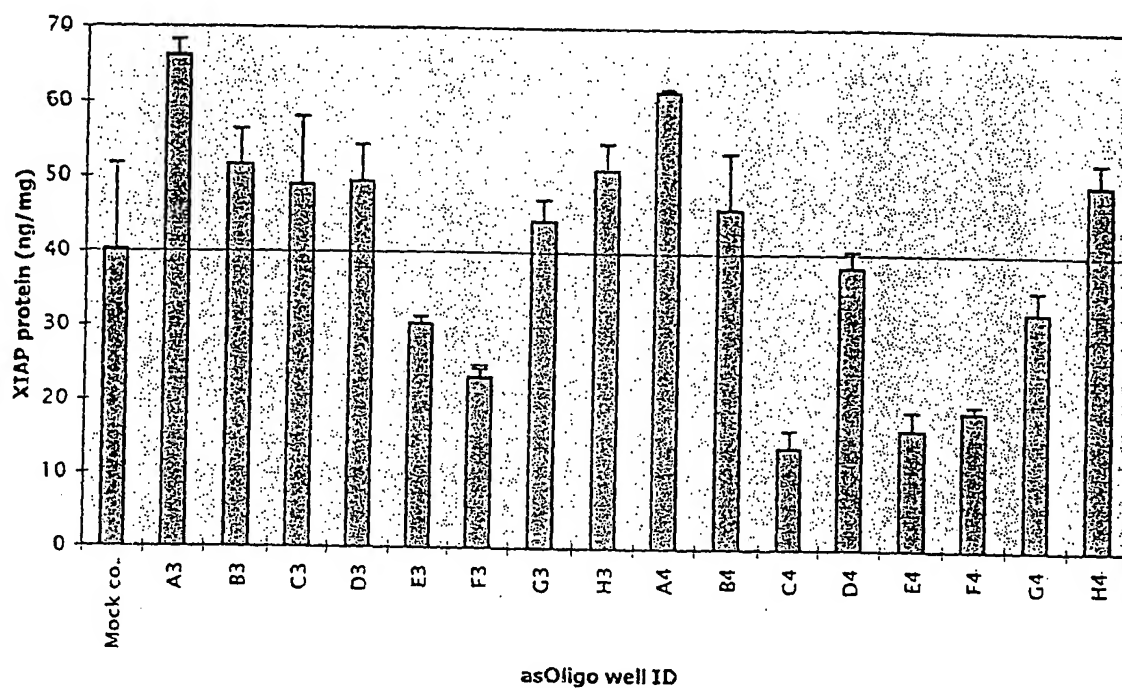


Fig. 7C

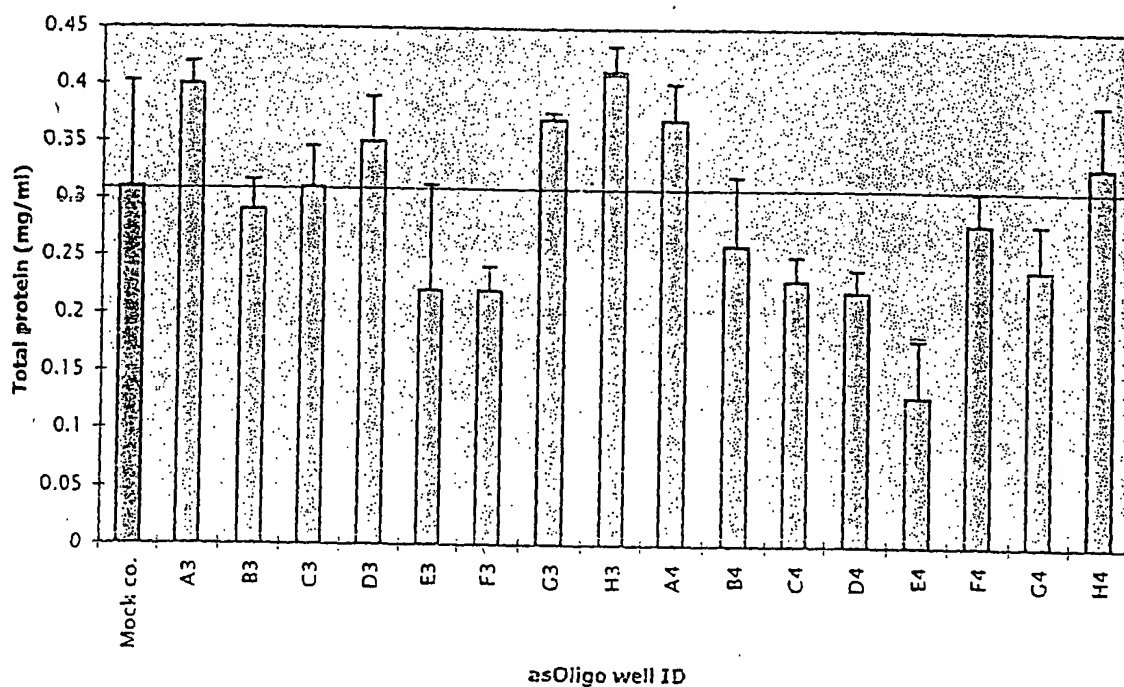


Fig. 7D

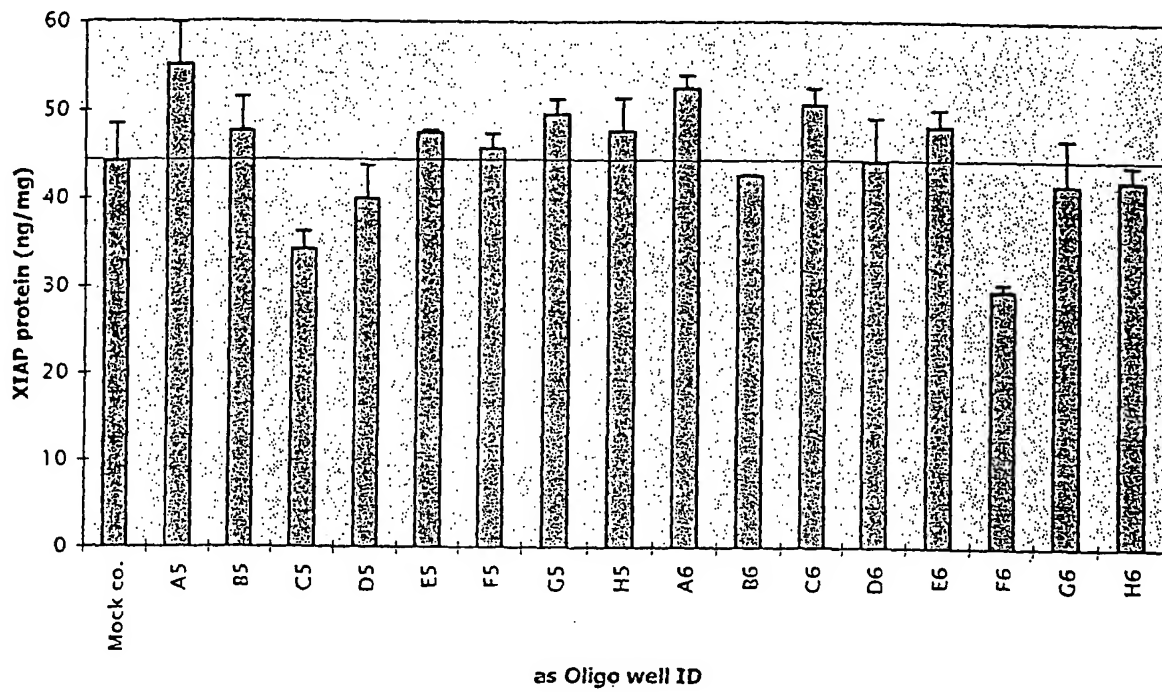


Fig. 7E

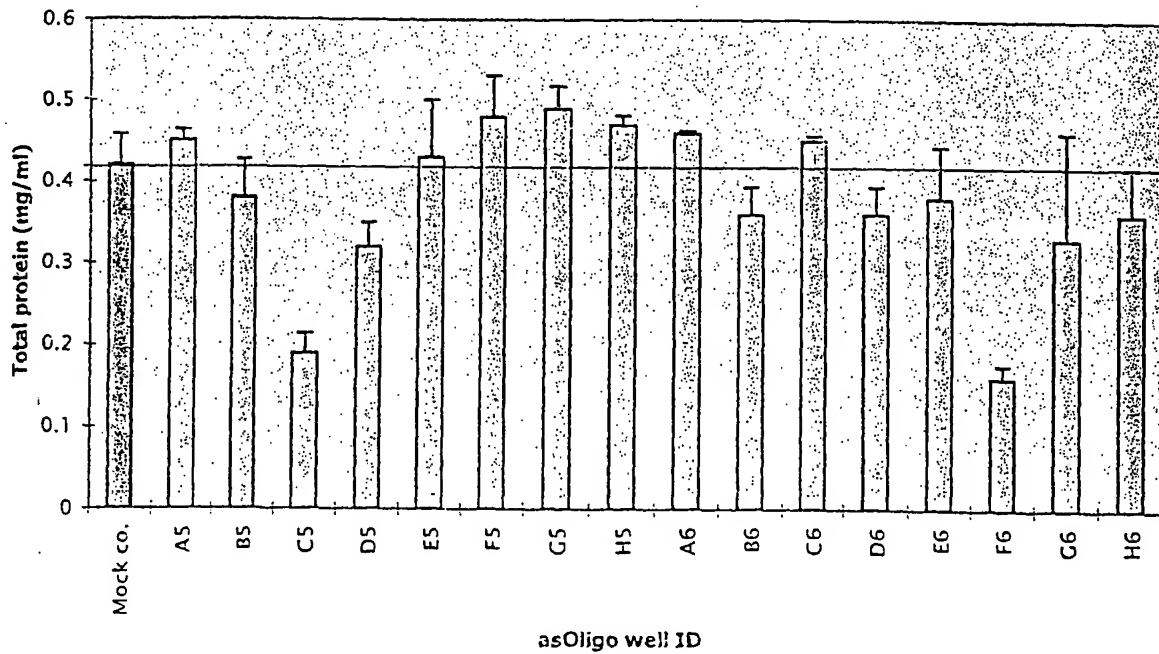


Fig. 7F

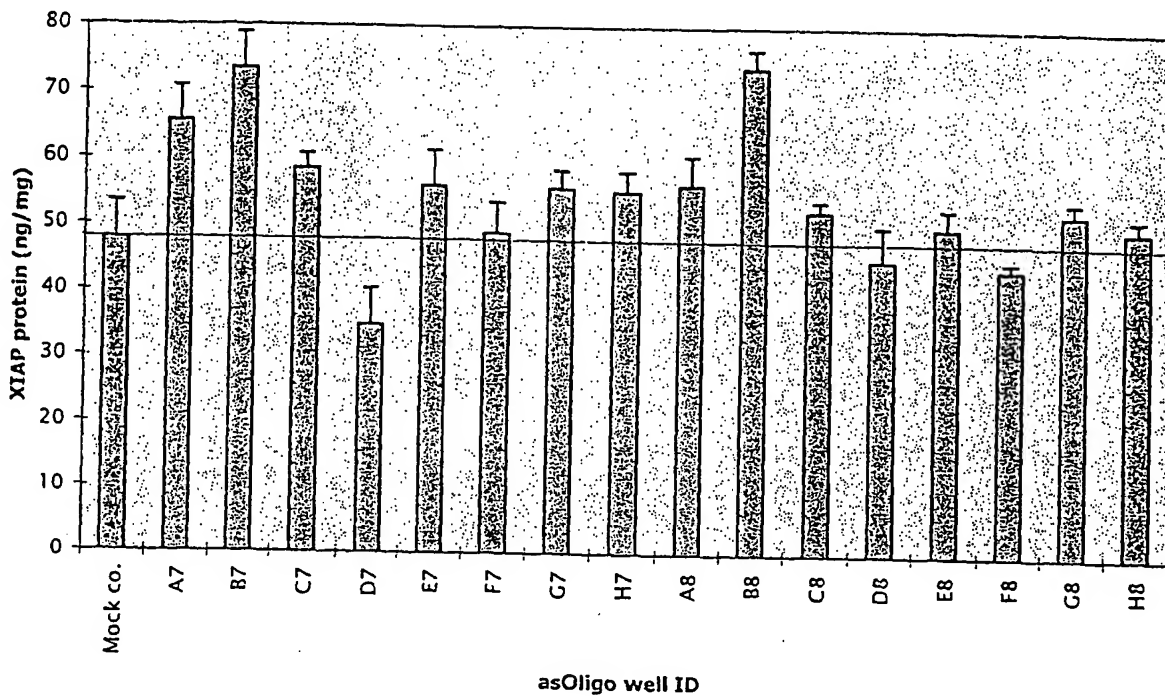


Fig. 7G

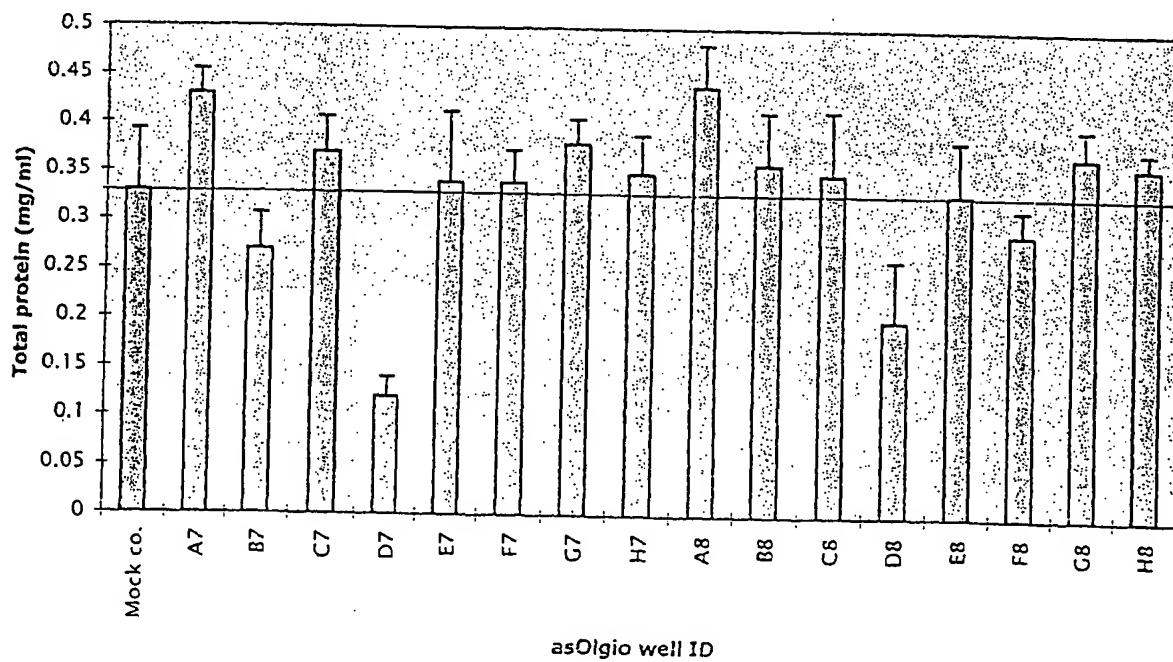


Fig. 7H

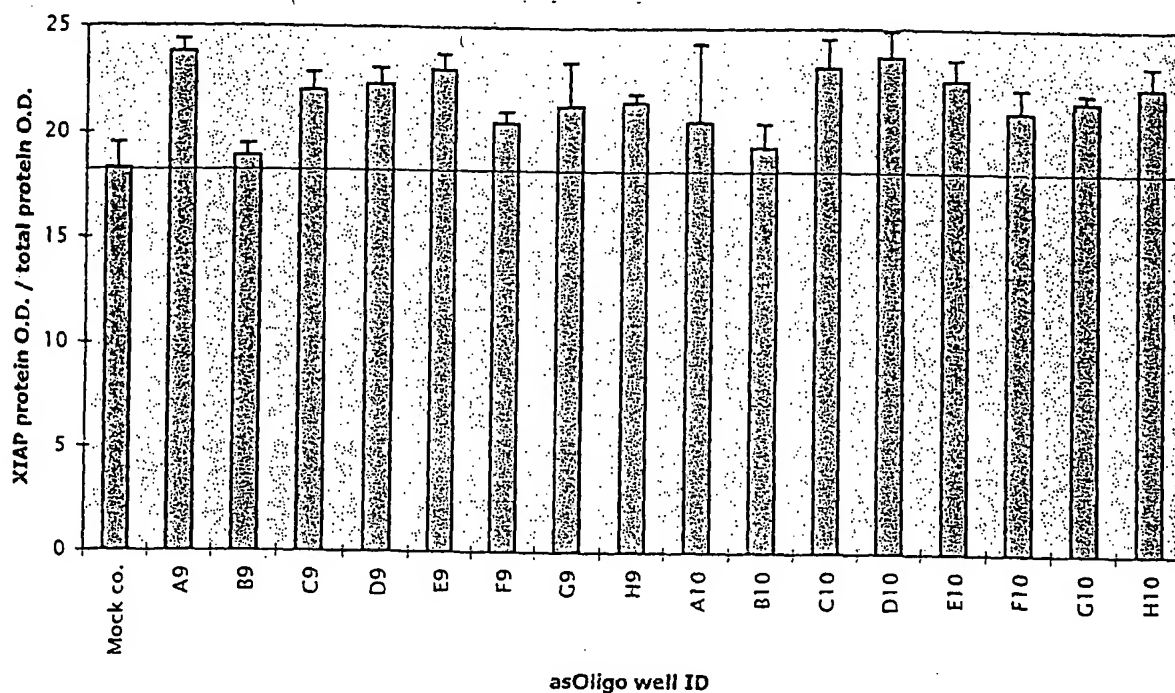


Fig. 7I

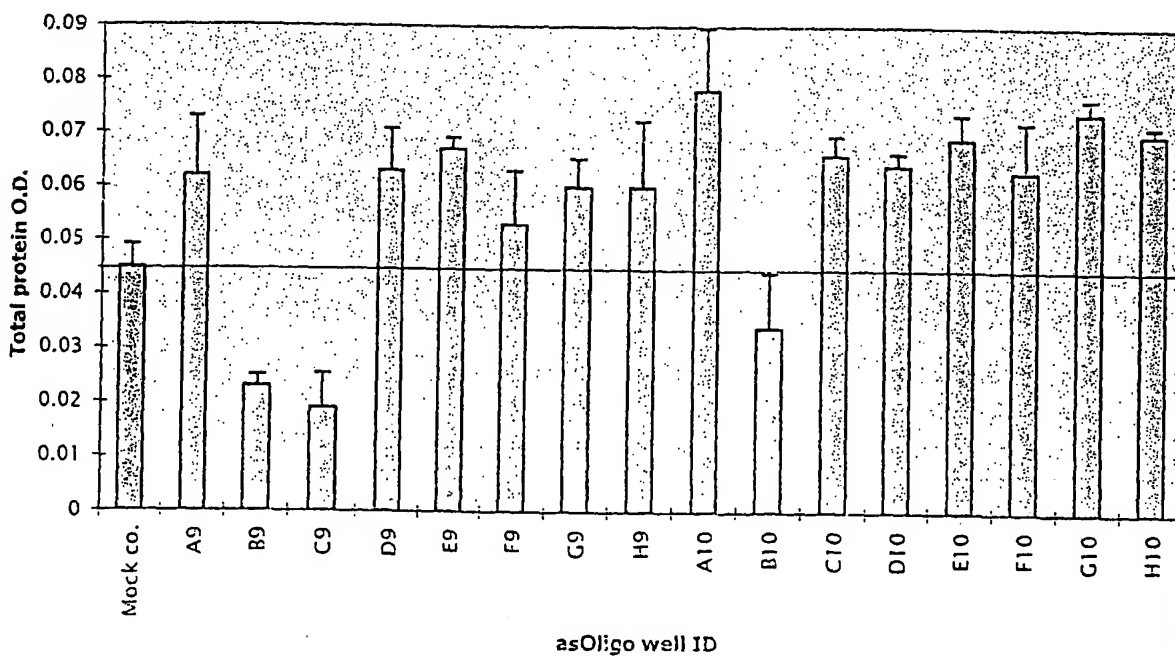


Fig. 7J

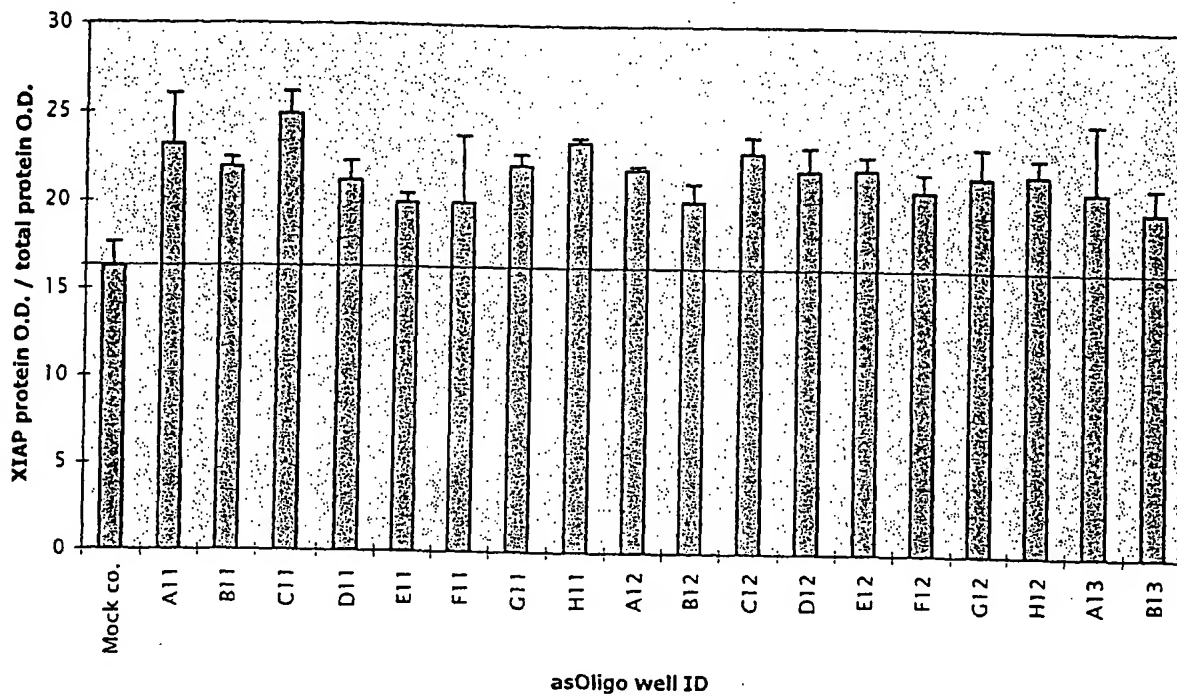


Fig. 7K

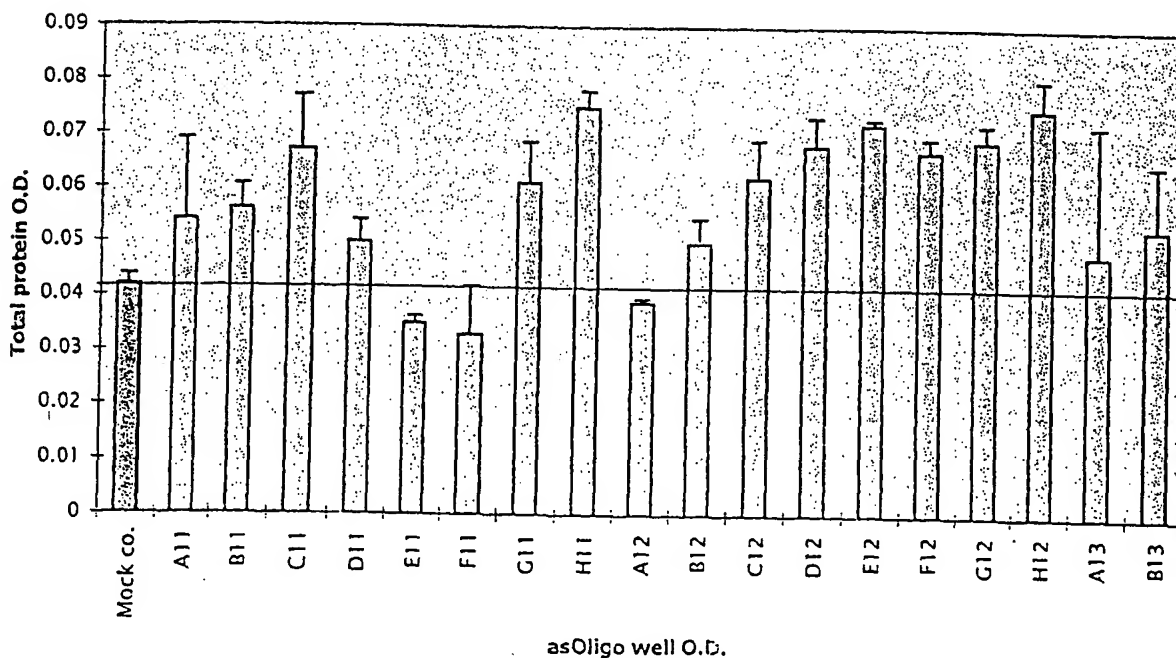


Fig. 7L

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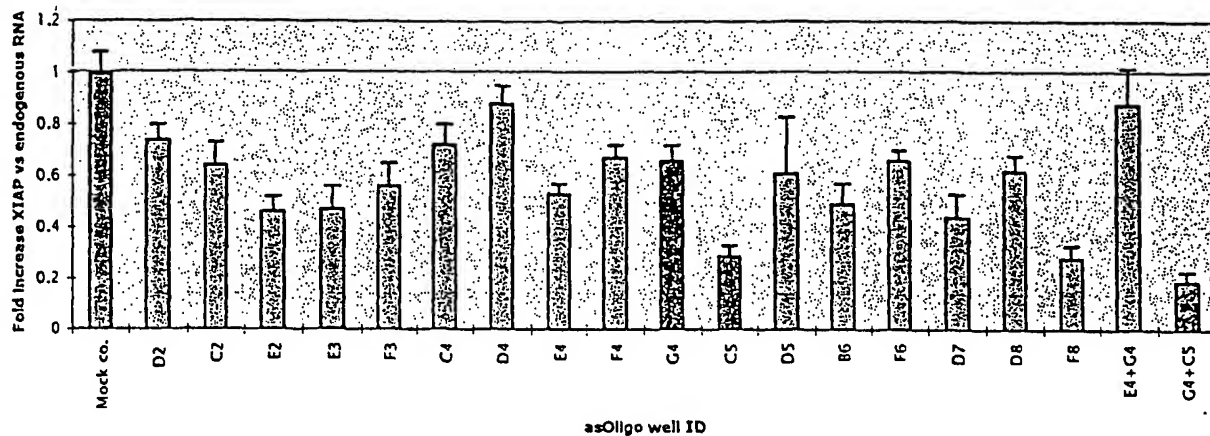


Fig. 8A

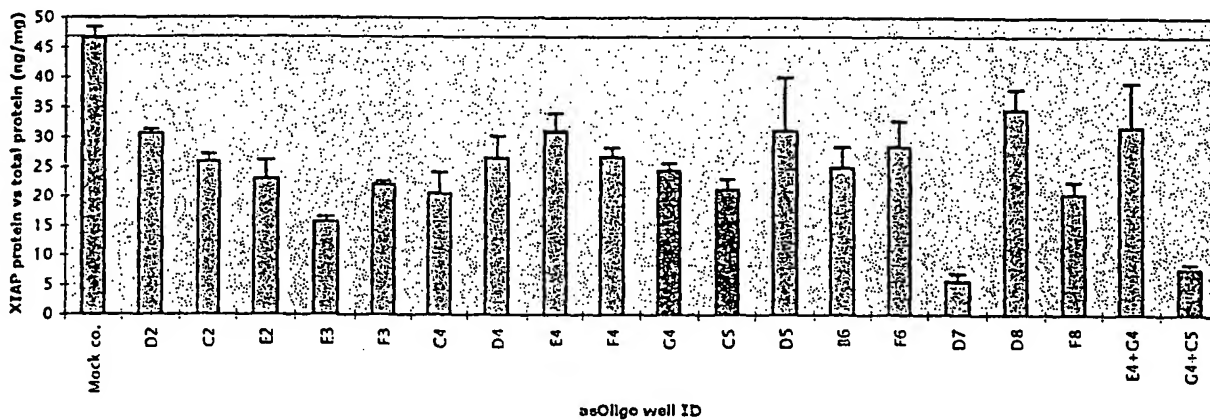


Fig. 8B

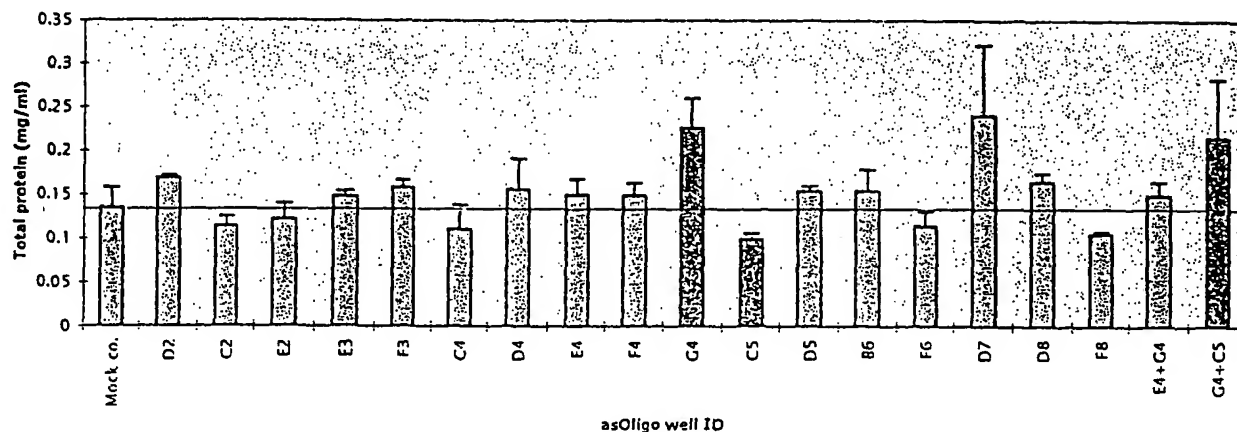


Fig. 8C

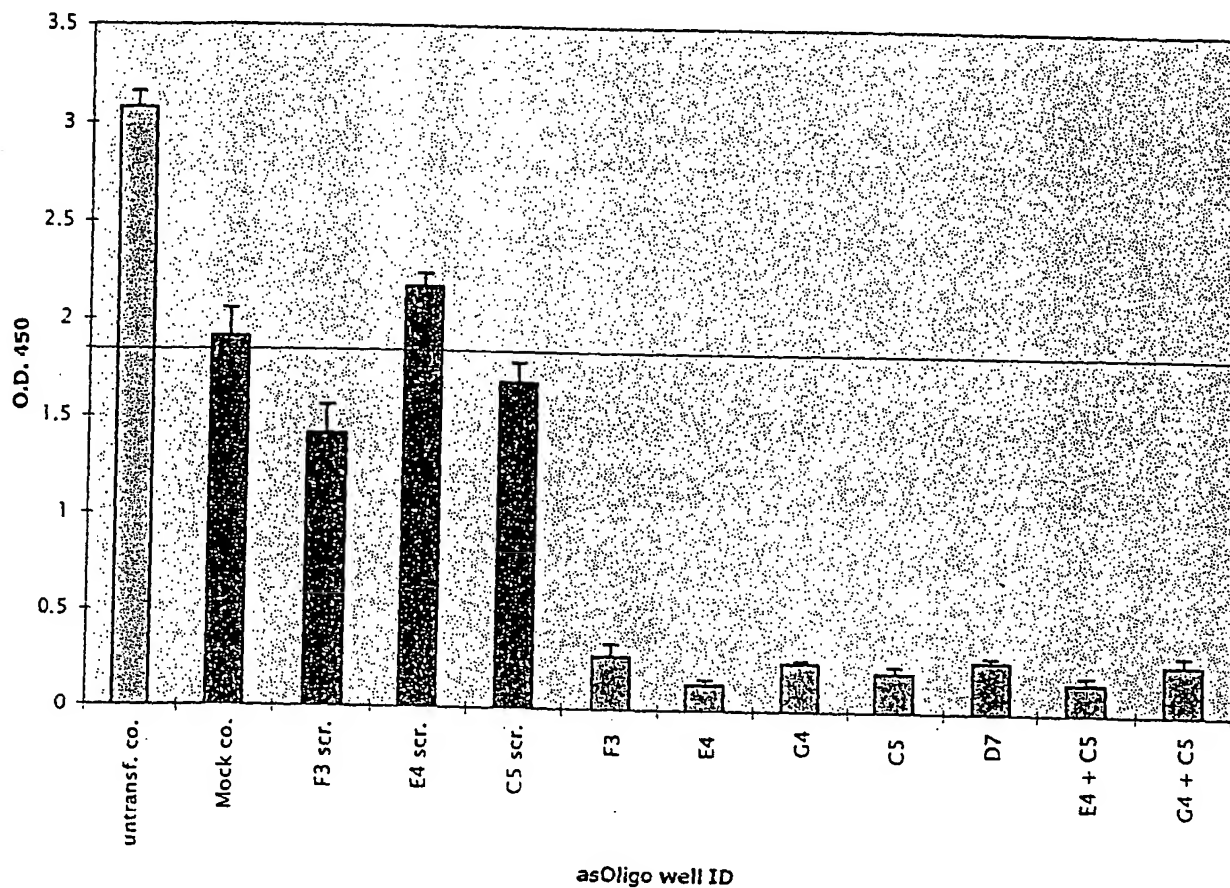


Fig. 9A

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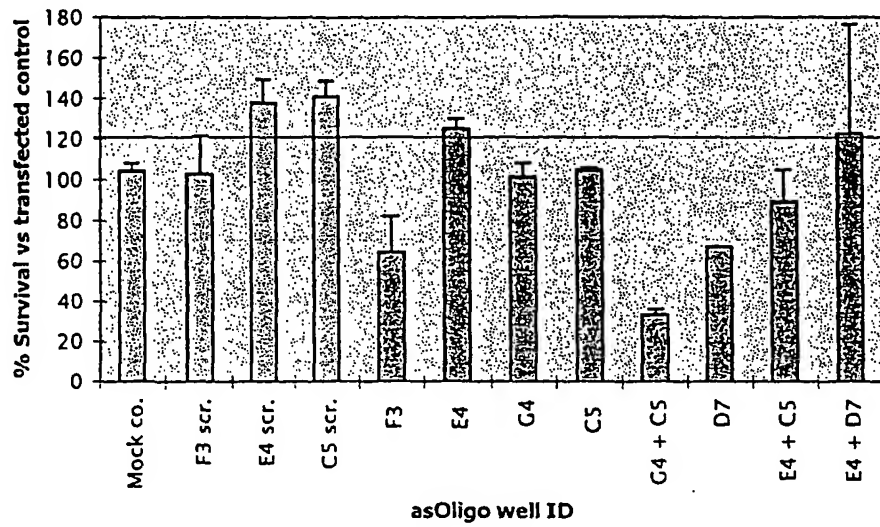


Fig. 9B

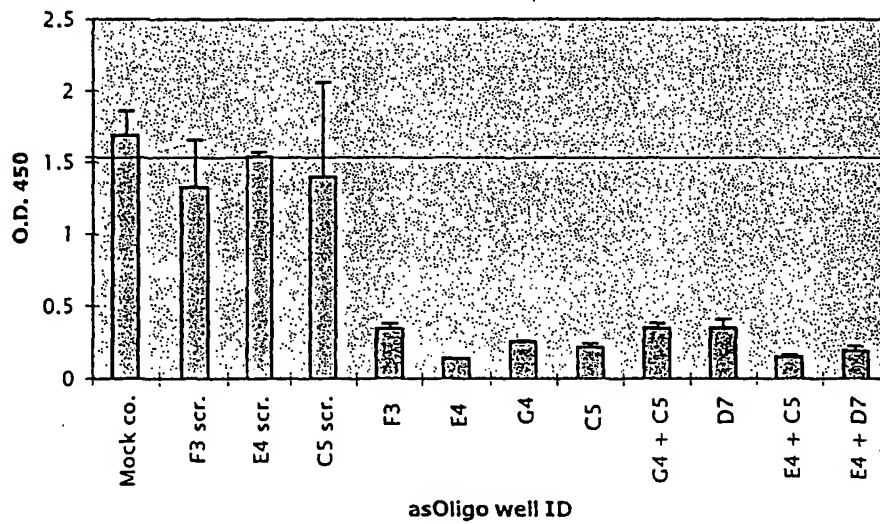
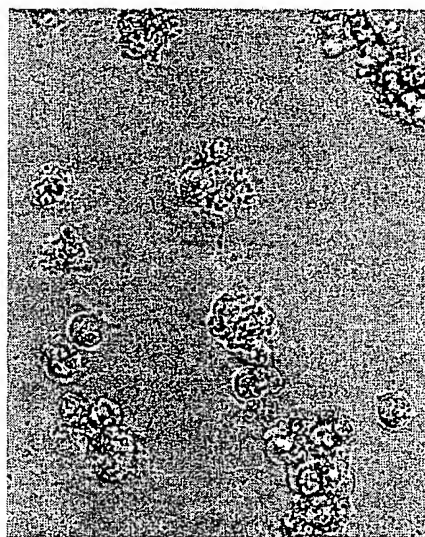
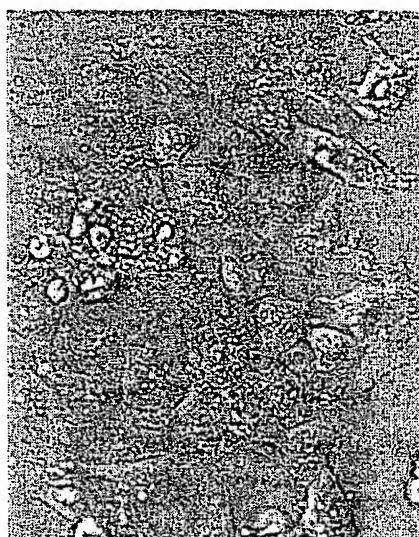


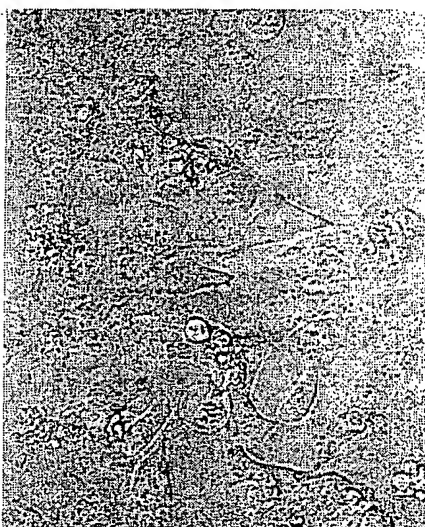
Fig. 9C



E4 AS, 1 uM



E4 REV, 1 uM



Mock control



E4 MM, 1 uM



Untransfected control



E4 SCR, 1 uM

Fig. 9D

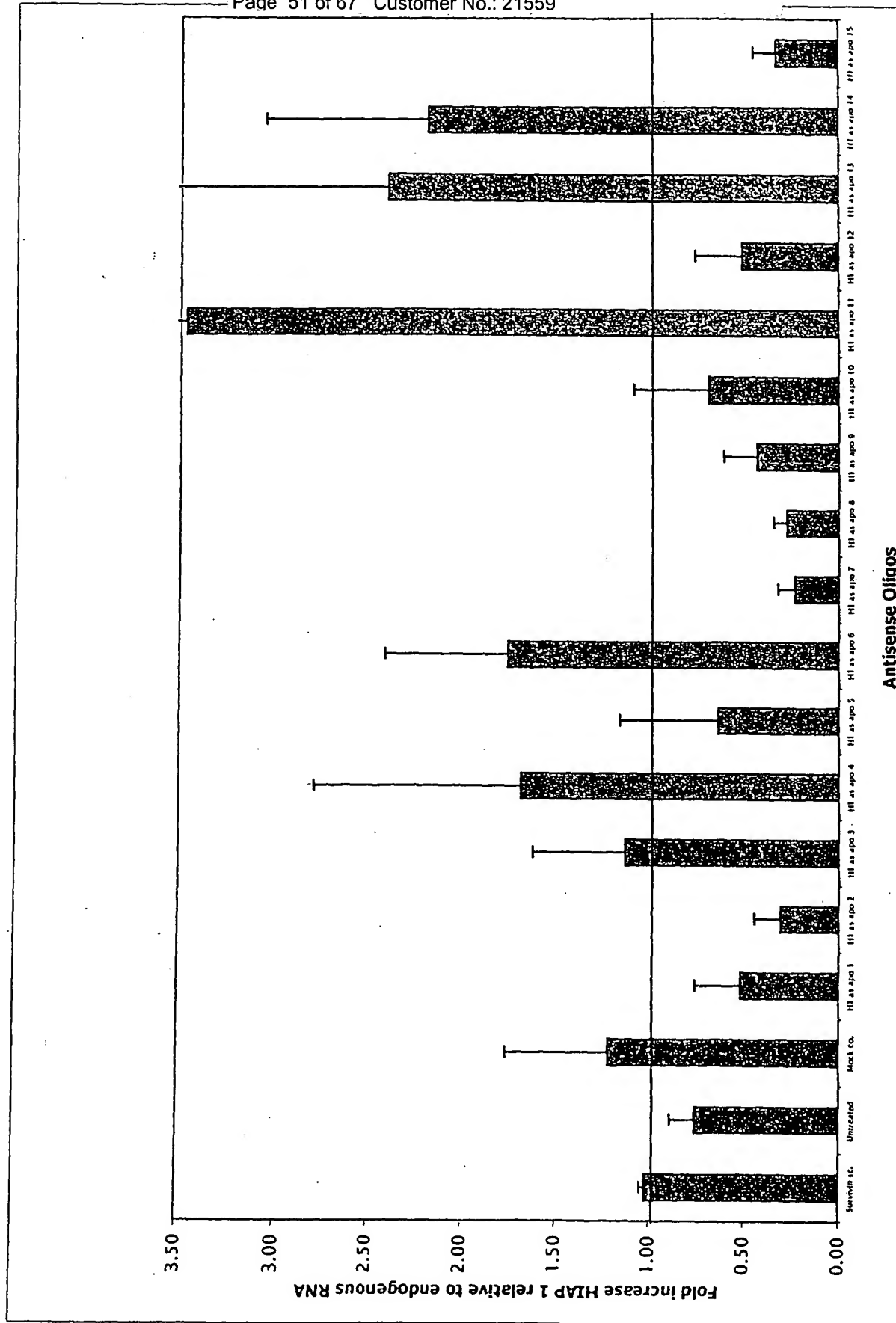


Fig. 10

Fig. 11A

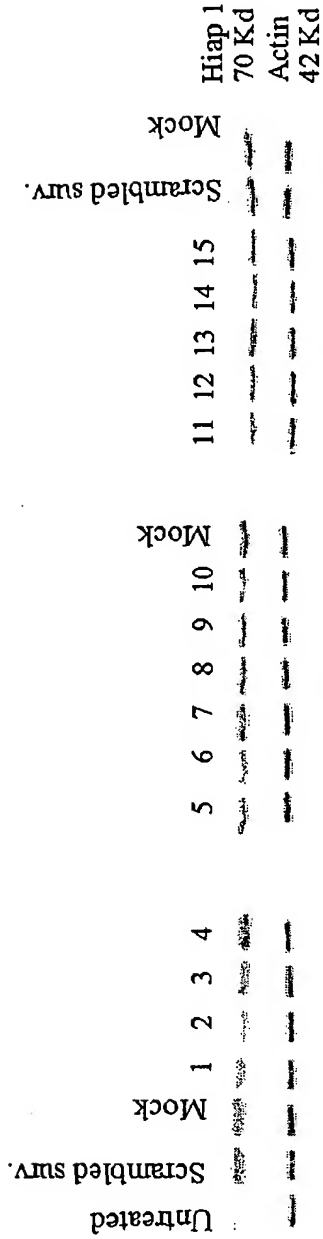
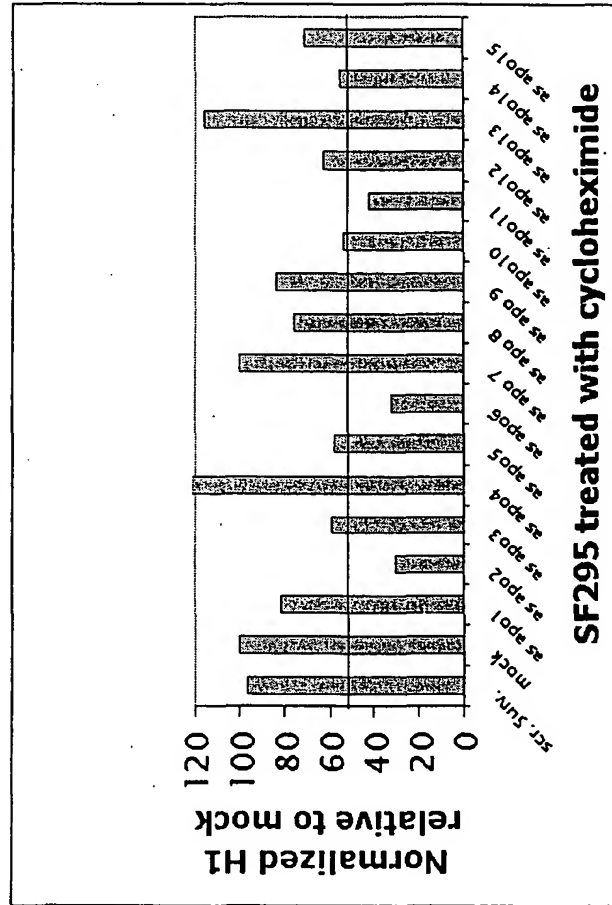


Fig. 11B



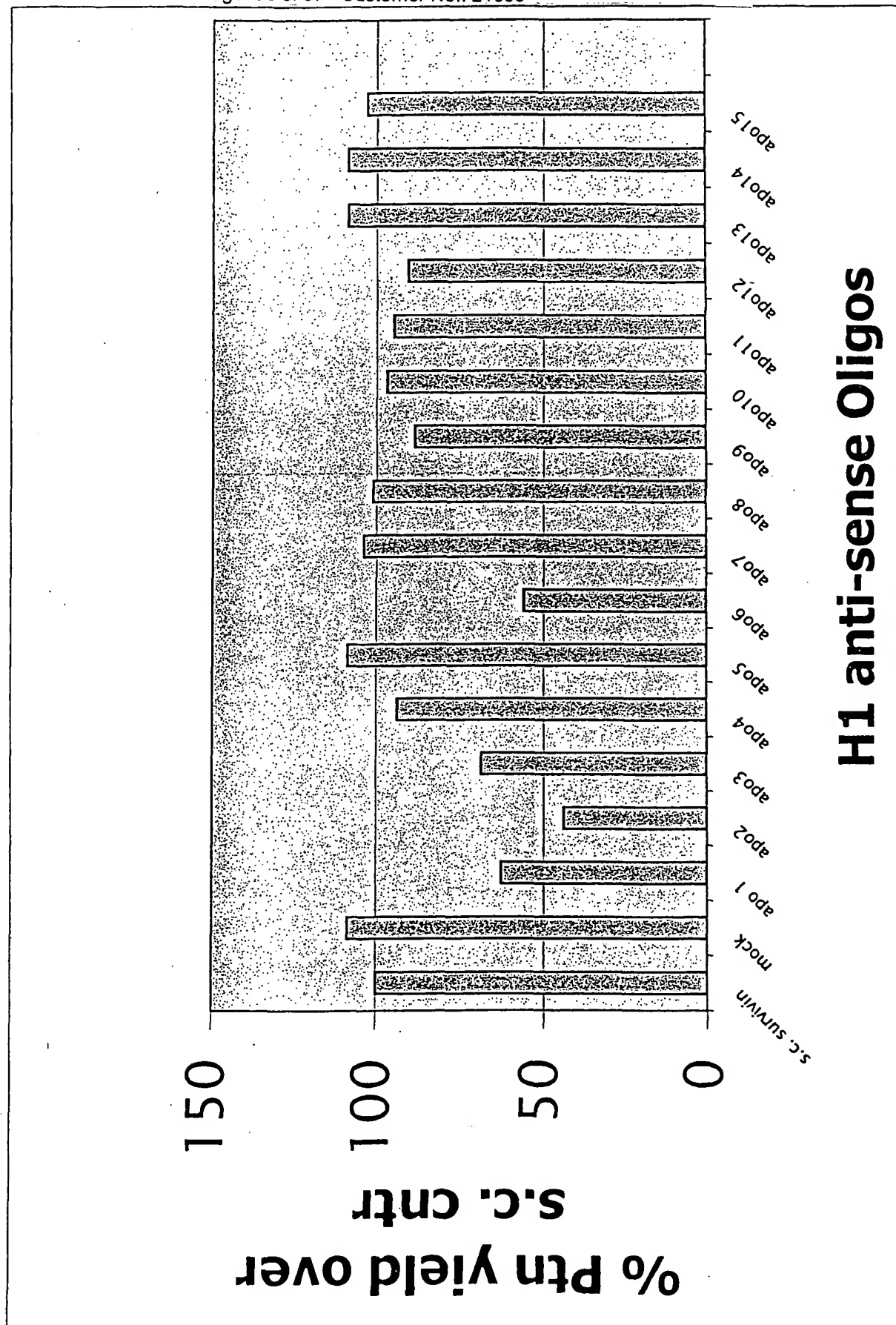


Fig. 12

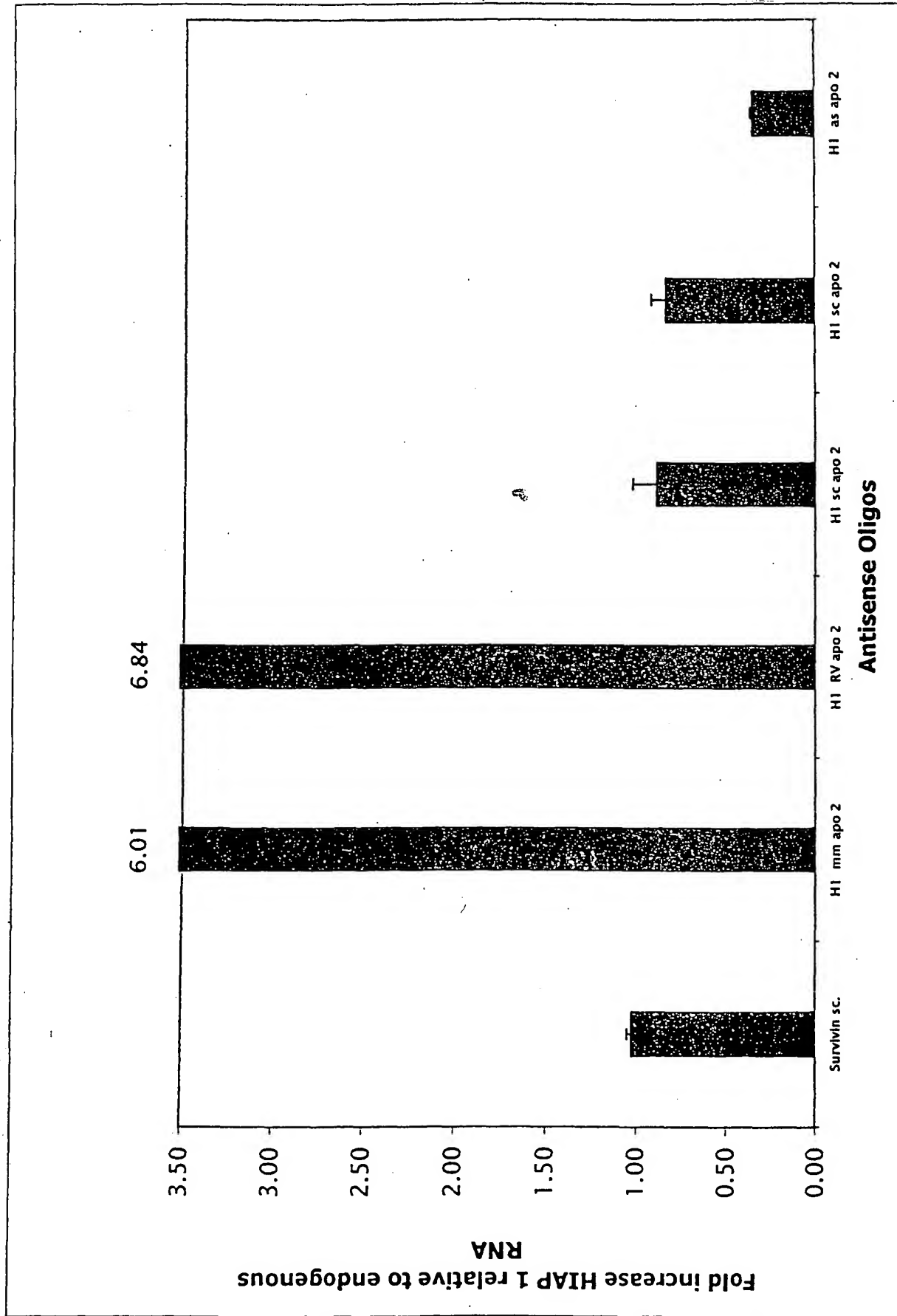


Fig. 13

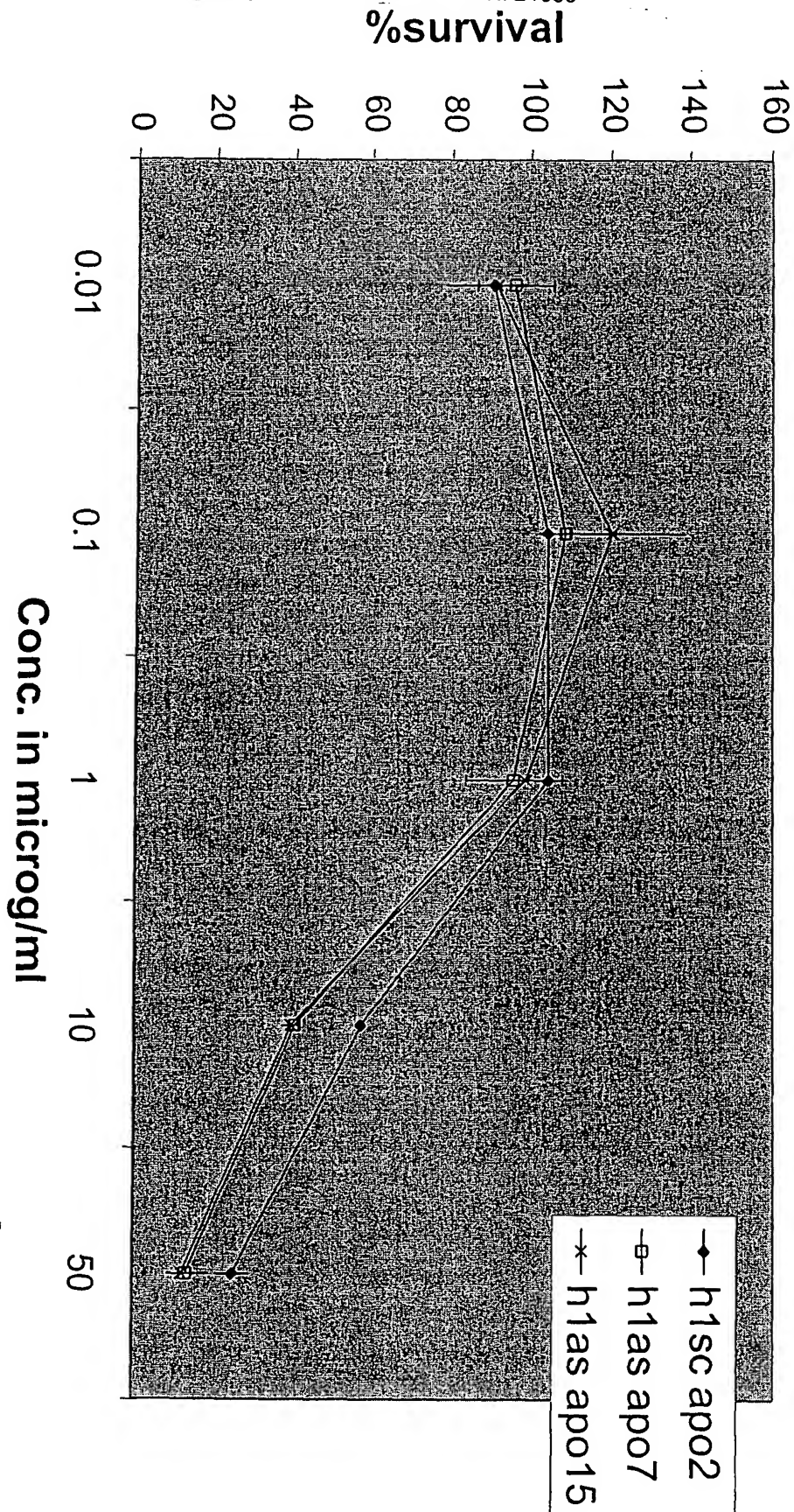


Fig. 14

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Applicant(s): Robert G. Korneluk et al.

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